Fig. 1A

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                                 M   A   P   P   A   A   R   L   A   L   L       11
GTCGACCCACGCGTCCGCCCACGCGTCCGGCCC ATG GCG CCG CCC GCC GCC CGC CTC GCC CTG CTC   66

  S   A   A   A   L   T   L   A   A   R   P   A   P   S   P   G   L   G   P   G   31
TCC GCC GCG GCG CTC ACG CTG GCG GCC CGG CCC GCG CCT AGC CCC GGC CTC GGC CCC GGA  126

  P   E   C   F   T   A   N   G   A   D   Y   R   G   T   Q   N   W   T   A   L   51
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA  186

  Q   G   G   K   P   C   L   F   W   N   E   T   F   Q   H   P   Y   N   T   L   71
CAA GGC GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG  246

  K   Y   P   N   G   E   G   G   L   G   E   H   N   Y   C   R   N   P   D   G   91
AAA TAC CCC AAC GGG GAG GGG GGC CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA  306

  D   V   S   P   W   C   Y   V   A   E   H   E   D   G   V   Y   W   K   Y   C   111
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT  366

  E   I   P   A   C   Q   M   P   G   N   L   G   C   Y   K   D   H   G   N   P   131
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA  426

  P   P   L   T   G   T   S   K   T   S   N   K   L   T   I   Q   T   C   I   S   151
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT  486

  F   C   R   S   Q   R   F   K   F   A   G   M   E   S   G   Y   A   C   F   C   171
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGG ATG GAG TCA GGC TAT GCT TGC TTC TGT  546

  G   N   N   P   D   Y   W   K   Y   G   E   A   A   S   T   E   C   N   S   V   191
GGA AAC AAT CCT GAT TAC TGG AAG TAC GGG GAG GCA GCC AGT ACC GAA TGC AAC AGC GTC  606

  C   F   G   D   H   T   Q   P   C   G   G   D   G   R   I   I   L   F   D   T   211
TGC TTC GGG GAT CAC ACC CAA CCC TGT GGT GGC GAT GGC AGG ATC ATC CTC TTT GAT ACT  666

  L   V   G   A   C   G   G   N   Y   S   A   M   S   S   V   V   Y   S   P   D   231
CTC GTG GGC GCC TGC GGT GGG AAC TAC TCA GCC ATG TCT TCT GTG GTC TAT TCC CCT GAC  726

  F   P   D   T   Y   A   T   G   R   V   C   Y   W   T   I   R   V   P   G   A   251
TTC CCC GAC ACC TAT GCC ACG GGG AGG GTC TGC TAC TGG ACC ATC CGG GTT CCG GGG GCC  786

  S   H   I   H   F   S   F   P   L   F   D   I   R   D   S   A   D   M   V   E   271
TCC CAC ATC CAC TTC AGC TTC CCC CTA TTT GAC ATC AGG GAC TCG GCG GAC ATG GTG GAG  846

  L   L   D   G   Y   T   H   R   V   L   A   R   F   H   G   R   S   R   P   P   291
CTT CTG GAT GGC TAC ACC CAC CGT GTC CTA GCC CGC TTC CAC GGG AGG AGC CGC CCA CCT  906

  L   S   F   N   V   S   L   D   F   V   I   L   Y   F   F   S   D   R   I   N   311
CTG TCC TTC AAC GTC TCT CTG GAC TTC GTC ATC TTG TAT TTC TTC TCT GAT CGC ATC AAT  966

  Q   A   Q   G   F   A   V   L   Y   Q   A   V   K   E   E   L   P   Q   E   R   331
CAG GCC CAG GGA TTT GCT GTT TTA TAC CAA GCC GTC AAG GAA GAA CTG CCA CAG GAG AGG  1026

  P   A   V   N   Q   T   V   A   E   V   I   T   E   Q   A   N   L   S   V   S   351
CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC  1086

  A   A   R   S   S   K   V   L   Y   V   I   T   T   S   P   S   H   P   P   Q   371
GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG  1146

  T   V   P   G   S   N   S   W   A   P   P   M   G   A   G   S   H   R   V   E   391
ACT GTC CCA GGT AGC AAT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA  1206

  G   W   T   V   Y   G   L   A   T   L   L   I   L   T   V   T   A   I   V   A   411
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GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC CTC ACA GTC ACA GCC ATT GTA GCA   1266

  K   I   L   L   H   V   T   F   K   S   H   R   V   P   A   S   G   D   L   R     431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG   1326

  D   C   H   Q   P   G   T   S   G   E   I   W   S   I   F   Y   K   P   S   T     451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT   1386

  S   I   S   I   F   K   K   K   L   K   G   Q   S   Q   Q   D   D   R   N   P     471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC   1446

  L   V   S   D   *     476
CTT GTG AGT GAC TAA   1461
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AAACCCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC   1540

TGACAGACTCTTCCCTCCTCTCCCTCTGCCTCGGCCTCTTCGGGGAAACCCTCCTCCTACAGACTAGGAAGAGGCACC   1619

TGCTGCCAGGGCAGGCAGAGCCTGGATTCCTCCTGCTT   1657

Fig_1B

Fig. 1C

GTCGACCCACGCGTCCGCCCGGCTCCCGGTGCTGCCCCCTCTGCCCCGGGCCGCGCCCGGGGGTCCCGCACTGACGGCC   79

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       M   A   P   P   A   A   R   L   A   L   L   S   A   A   A   L   T   L   A       19
C  ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG      137

   A   R   P   A   P   G   P   R   S   G   P   E   C   F   T   A   N   G   A   D       39
GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT      197

   Y   R   G   T   Q   S   W   T   A   L   Q   G   G   K   P   C   L   F   W   N       59
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC      257

   E   T   F   Q   H   P   Y   N   T   L   K   Y   P   N   G   E   G   G   L   G       79
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC      317

   E   H   N   Y   C   R   N   P   D   G   D   V   S   P   W   C   Y   V   A   E       99
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG      377

   H   E   D   G   V   Y   W   K   Y   C   E   I   P   A   C   Q   M   P   G   N      119
CAT GAG GAC GGA GTC TAC TGG AAG TAC TGT GAA ATT CCT GCC TGC CAG ATG CCT GGA AAC      437

   L   G   C   Y   K   D   H   G   N   P   P   P   L   T   G   T   S   K   T   S      139
CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA CCT CCT CTC ACG GGC ACC AGT AAA ACC TCT      497

   N   K   L   T   I   Q   T   C   I   S   F   C   R   S   Q   R   F   K   F   A      159
AAC AAG CTC ACC ATA CAA ACC TGT ATC AGC TTC TGT CGG AGT CAG AGA TTC AAG TTT GCT      557

   G   M   E   S   G   Y   A   C   F   C   G   N   N   P   D   Y   W   K   H   G      179
GGG ATG GAG TCA GGC TAT GCC TGC TTC TGT GGG AAC AAT CCT GAC TAC TGG AAG CAC GGG      617

   E   A   A   S   T   E   C   N   S   V   C   F   G   D   H   T   Q   P   C   G      199
GAG GCG GCC AGC ACC GAG TGC AAT AGT GTC TGC TTC GGG GAC CAC ACG CAG CCC TGC GGT      677

   G   D   G   R   I   I   L   F   D   T   L   V   G   A   C   G   G   N   Y   S      219
GGG GAC GGC AGG ATT ATC CTC TTT GAC ACT CTC GTG GGC GCC TGC GGT GGG AAC TAC TCA      737

   A   M   A   A   V   V   Y   S   P   D   F   P   D   T   Y   A   T   G   R   V      239
GCC ATG GCA GCC GTG GTG TAC TCC CCT GAC TTC CCT GAC ACC TAC GCC ACT GGC AGA GTC      797

   C   Y   W   T   I   R   V   P   G   A   S   R   I   H   F   N   F   T   L   F      259
TGC TAC TGG ACC ATC CGG GTT CCA GGA GCC TCT CGC ATC CAT TTC AAC TTC ACC CTG TTT      857

   D   I   R   D   S   A   D   M   -V   E   L   L   D   G   Y   T   H   R   V   L      279
GAT ATC AGG GAC TCT GCA GAC ATG GTG GAG CTG CTG GAC GGC TAC ACC CAC CGC GTC CTG      917

   V   R   L   S   G   R   S   R   P   P   L   S   F   N   V   S   L   D   F   V      299
GTC CGG CTC AGT GGG AGG AGC CGC CCG CCT CTG TCT TTC AAT GTC TCT CTG GAT TTT GTC      977

   I   L   Y   F   F   S   D   R   I   N   Q   A   Q   G   F   A   V   L   Y   Q      319
ATT TTG TAT TTC TTC TCT GAT CGC ATC AAT CAG GCC CAG GGA TTT GCT GTG TTG TAC CAA     1037

   A   T   K   E   E   P   P   Q   E   R   P   A   V   N   Q   T   L   A   E   V      339
GCC ACC AAG GAG GAA CCG CCA CAG GAG AGA CCT GCT GTC AAC CAG ACC CTG GCA GAG GTG     1097

   I   T   E   Q   A   N   L   S   V   S   A   A   H   S   S   K   V   L   Y   V      359
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        ATC ACC GAG CAA GCC AAC CTC AGT GTC AGC GCT GCC CAC TCC TCC AAA GTC CTC TAT GTC  1157

     I    T    P    S    P    S    H    P    P    Q    T    A    Q    V    A    I    P    G    H    R   379
        ATC ACC CCC AGC CCC AGC CAC CCT CCG CAG ACT GCC CAG GTA GCC ATT CCT GGG CAC CGT  1217

     Q    L    G    P    T    A    E    W    K    D    G    L    C    T    A    W    R    P    S   399
        CAG TTG GGG CCA ACA GCC ACA GAG TGG AAG GAT GGA CTG TGT ACG GCC TGG CGA CCC TCC  1277

     S    S    S    Q    S    Q    Q    L    S    Q    R    F    F    C    M    S    H    L    N    L   419
        TCA TCC TCA CAG TCA CAG CAG TTG TCG CAA AGA TTC TTC TGC ATG TCA CAT TTA AAT CTC  1337

     I    E    S    L    H    Q    E    T    L    G    T    V    V    S    L    G    L    L    E    I   439
        ATC GAG TCC CTG CAT CAG GAG ACC TTA GGG ACT GTC GTC AGC CTG GGG CTT CTG GAG ATA  1397

     S    G    P    F    S    M    N    L    P    L    Q    S    P    S    L    R    R    S    S    R   459
        TCT GGA CCA TTT TCT ATG AAC CTT CCA CTA CAA TCT CCA TCT TTA AGA AGA AGC TCA AGG  1457

     V    R    V    N    K    M    T    A    I    P    S    *                                   471
        GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA                                     1493
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GTGACTGAAGCCCACGCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCTGAGTTCTCCTCTGATGAGTTC 1572

CCTGCCTTCCCATTCACCACCATCTCTTTTGGGAGCACCCTGCTTTAGAGGCAGCCCAGCCTGGGATCCTCCATCACAT 1651

GTACCAGCCTGGCTGCTCTGCTGGGGATGGTAAGACAGGCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730

CTCTTGGGTGGTGGGGAGGTATAGTGTAGGATGAGTTTTCTTGCTTCTTCTCTGTTTTGTCCACATACAGATCGGTTTC 1809

CCGTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAGGTTTTCTAGGCTGGCCTGGTTCCCCACTAAGA 1888

GTGGCATTGGCGCCCTAGAGGCCCAGAGGCCCAGTGTAGGCTTGGAGCTTTCTCTGCTGCCAACTACCATGTGTCATCT 1967

AGTCCGAGGGGACTGAGAGCAGGGCCACACCAGATGTCATCTTTCTAGAGGGTTCTTTTTAGTACCCACTGACCAATGG 2046

GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACAGACACAGTGAACTTCCTGGATACTAGACTTAACTAGCC 2125

TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAATTCAGCCTGTCTTCCTGTCCTCAGCCCAAGCCTGTAGCCTAG 2204

AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283

TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362

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AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTGTCCCCCAGACAGGGAGGCAGGAAAAGGTCAGGCTTGGGAACTGGA 2678

GATCCTCCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGGCCATCCCCGACTGAGAAGTC 2757

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GCCTCTGCTCTCCTGGGTACCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCTC 2915

TCCTCTAGCTGCTGCTCCCCAGGACTGTCTGGGGCCATCTGGGGATCAGGGAGAGGCAGCAGGAGTACTGACGAGGCAG 2994

TGACCTGAGCTGATGAGTCAACCAGAGGACACCAGAGTCTACAGTGGGCTGGCTGCTGGCTCAGCTCCTATGGGAGGCC   3073

TACAGGGGTACTAAGCTAGGGGGTCATCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC   3152

CACTACATAAGAAGACCACTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC   3231

CCCTGAGACCAAGTGTTGAGTCACAGAGTGCCATGTGCGTAGTGCATAAAGGATATGGGTTCTTAACCAGGGAAGGCTC   3310

ATAGCAGGCCAGGACATTTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACTCACCTGTCTCTTCCT   3389

ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGTGGCAGCTGCGGCTCAGCATTGGTGTCCCCAGGAAGGGCGGTGGATG   3468

TGCCCACGCTCCTTTTGCTGTGGGCCTGGCACAGCCCAACACTGCAGGGCCCACCTTCTCTCTTGGGGGGTAGGGACAC   3547

ATAAGGAAAACTAACCCACCTCCAACAACAGCAGAGGACAGTGGGAAGGAAGGGCTGTAAATCACCCAGGCCAGACCTC   3626

CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCTGCCTG   3705

GAGCATAGGGGTAAGCCGAGGGAGAAGAGCAGCCCTCAGAGACATCAGCTAAAAACATAGGTGCCCTATGTCCCTCCCT   3784

TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCCACATCAGCAAGGATAGGGCT   3863

GCGGCTGCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA   3942

AAAGCTCTTGAAGATCAAAGCTCTGGCGGGTACAGCTGTCCTGGCCTGTGGGCCAGCCCATGGGATGTGCCTGGGCCAG   4021

GTGCCACCCCACGGCTCACTGTCATCCCAGGAGGGACCCCACCTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA   4100

GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA   4179

CTCTGTCAGCCTCTGCAGGGGCCACACAAGTCTCCCGAGCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCTCCT   4258

GTGGAGTGTCCTGTTTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACTGCTAACCTCCGATTGGTCCCTTTGT   4337

GTCTCTGTTTACTGTCCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGCTGGGAGTGGGGGGTGGGGATGCT   4416

GGCTGCACCCCCACCCTGGTCTGCCAACAGAACCTGGGGGCCTCACACGGGCTCCTGTCTTGCCAAGCTGGAGCTGAGC   4495

ACACTGGCCCAGGCTGAGTGGGGCAGAGCAAACAAGTGGAAGGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT   4574

AGATCCAGCGAGGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCCTCCAGCAG   4653

GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAATAAGATAGAAACATCA   4732

TGTATTTTAAAATATAAAATGAAGTGTGACACACTGTATACAATTTAATATATATTTTTAGGATTTTGTTATTTAAGAA   4811

AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTTACTGTTTGAAGAAAATAAATATTCTCA   4890

TTGTTGTAGAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC   4928

Fig. 1E

```
                10        20        30        40        50        60        70
Hum  MAPPAARLALLSAAALTLAARPAPSPGLGPGPECFTANGADYRGTQNWTALQGGKPCLFWNETFQHPYNT
     :::::::::::::::::::::::::::::.: .::::::::::::::::::::::::::::::::::::::
Mur. MAPPAARLALLSAAALTLAARPAPGPR--SGPECFTANGADYRGTQSWTALQGGKPCLFWNETFQHPYNT
                10        20          30        40        50        60

                80        90        100       110       120       130       140
Hum  LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNPPPLTGTSKT
     :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Mur. LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNPPPLTGTSKT
        70        80        90        100       110       120       130

                150       160       170       180       190       200       210
Hum. SNKLTIQTCISFCRSQRFKFAGMESGYACFCGNNPDYWKYGEAASTECNSVCFGDHTQPCGGDGRIILFD
     :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Mur.  SNKLTIQTCISFCRSQRFKFAGMESGYACFCGNNPDYWKHGEAASTECNSVCFGDHTQPCGGDGRIILFD
     140       150       160       170       180       190       200

                220       230       240       250       260       270       280
Hum. TLVGACGGNYSAMSSVVYSPDFPDTYATGRVCYWTIRVPGASHIHFSFPLFDIRDSADMVELLDGYTHRV
     :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Mur.  TLVGACGGNYSAMAAVVYSPDFPDTYATGRVCYWTIRVPGASRIHFNFTLFDIRDSADMVELLDGYTHRV
     210       220       230       240       250       260       270

                290       300       310       320       330       340       350
Hum. LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQAVKEELPQERPAVNQTVAEVITEQANLSV
     :.:.. ::::::::::::::::::::::::::::::::::::::::.::: ::::::::::.:::::::::::
Mur. LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQATKEEPPQERPAVNQTLAEVITEQANLSV
     280       290       300       310       320       330       340

                360       370       380       390       400       410       420
Hum  SAARSSKVLYVITTSPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK
     :::.:::::::::.: :::::::::.  ::.     :.   : :.: :: :: .
Mur. SAAHSSKVLYVITPSPSHPPQTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSQSQQLSQRFFCM
     350       360       370       380       390       400       410

                430       440       450       460       470
Hum. SHRVPASGDLRDCHQPGTSGEIWSIFYKPSTSISIFKKKLKGQSQ-QDDRNPLVSD
     ::  .  .   :: . .  .  :  : .... :.  .. :.  .   ...
Mur. SHLNLIESLHQETLGTVVSLGLLEISGPFSMNLPLQSPSLRRSSRVRVNKMTAIPS
        420       430       440       450       460       470
```

Fig. IF

Fig. 1G
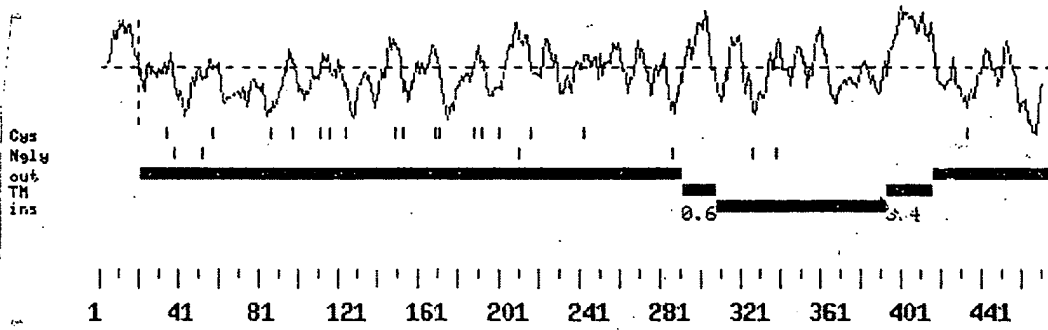
Fig. 1H
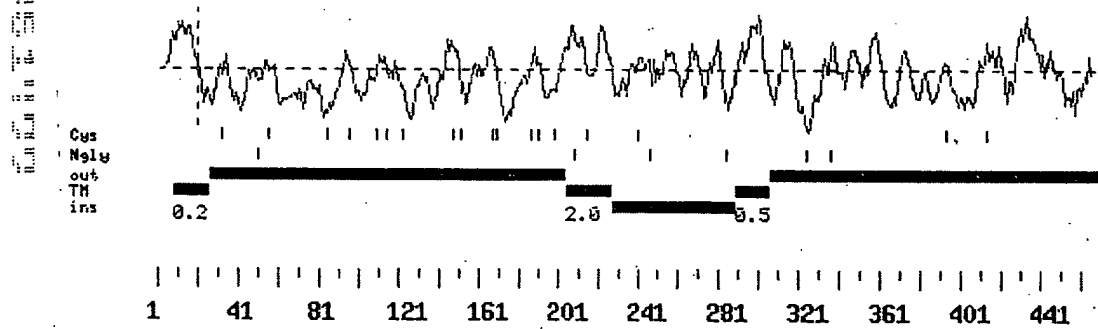
Fig. 2A

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                              M   M   L   P   Q   N   S   W   H   I   D   F   G     13
GCGGCCGCTCGCGATCTAGAACTAGTA ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA   66

  R   C   C   C   H   Q   N   L   F   S   A   V   V   T   C   I   L   L   L   N    33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GTG GTA ACT TGC ATC CTG CTC CTG AAT  126

  S   C   F   L   I   S   S   F   N   G   T   D   L   E   L   R   L   V   N   G    53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA  186

  D   G   P   C   S   G   T   V   E   V   K   F   Q   G   Q   W   G   T   V   C    73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT  246

  D   D   G   W   N   T   T   A   S   T   V   V   C   K   Q   L   G   C   P   F    93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT  306

  S   F   A   M   F   R   F   G   Q   A   V   T   R   H   G   K   I   W   L   D   113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT  366

  D   V   S   C   Y   G   N   E   S   A   L   W   E   C   Q   H   R   E   W   G   133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA  426

  S   H   N   C   Y   H   G   E   D   V   G   V   N   C   Y   G   E   A   N   L   153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG  486

  G   L   R   L   V   D   G   N   N   S   C   S   G   R   V   E   V   K   F   Q   173
GGT TTG AGG CTA GTG GAT GGA AAC AAC TCC TGT TCA GGG AGA GTG GAG GTG AAA TTC CAA  546

  E   R   W   G   T   I   C   D   D   G   W   N   L   N   T   A   A   V   V   C   193
GAA AGG TGG GGG ACT ATA TGT GAT GAT GGG TGG AAC TTG AAT ACT GCT GCC GTG GTG TGC  606

  R   Q   L   G   C   P   S   S   F   I   S   S   G   V   V   N   S   P   A   V   213
AGG CAA CTA GGA TGT CCA TCT TCT TTT ATT TCT TCT GGA GTT GTT AAT AGC CCT GCT GTA  666

  L   R   P   I   W   L   D   D   I   L   C   Q   G   N   E   L   A   L   W   N   233
TTG CGC CCC ATT TGG CTG GAT GAC ATT TTA TGC CAG GGG AAT GAG TTG GCA CTC TGG AAT  726

  C   R   H   R   G   W   G   N   H   D   C   S   H   N   E   D   V   T   L   T   253
TGC AGA CAT CGT GGA TGG GGA AAT CAT GAC TGC AGT CAC AAT GAG GAT GTC ACA TTA ACT  786

  C   Y   D   S   S   D   L   E   L   R   L   V   G   G   T   N   R   C   M   G   273
TGT TAT GAT AGT AGT GAT CTT GAA CTA AGG CTT GTA GGT GGA ACT AAC CGC TGT ATG GGG  846

  R   V   E   L   K   I   Q   G   R   W   G   T   V   C   H   H   K   W   N   N   293
AGA GTA GAG CTG AAA ATC CAA GGA AGG TGG GGG ACC GTA TGC CAC CAT AAG TGG AAC AAT  906

  A   A   A   D   V   V   C   K   Q   L   G   C   G   T   A   L   H   F   A   G   313
GCT GCA GCT GAT GTC GTA TGC AAG CAG TTG GGA TGT GGA ACC GCA CTT CAC TTC GCT GGC  966

  L   P   H   L   Q   S   G   S   D   V   V   W   L   D   G   V   S   C   S   G   333
TTG CCT CAT TTG CAG TCA GGG TCT GAT GTT GTA TGG CTT GAT GGT GTC TCC TGC TCC GGT 1026

  N   E   S   F   L   W   D   C   R   H   S   G   T   V   N   F   D   C   L   H   353
AAT GAA TCT TTT CTT TGG GAC TGC AGA CAT TCC GGA ACC GTC AAT TTT GAC TGT CTT CAT 1086
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    Q   N   D   V   S   V   I   C   S   D   G   A   D   L   E   L   R   L   A   D   373
   CAA AAC GAT GTG TCT GTG ATC TGC TCA GAT GGA GCA GAT TTG GAA CTG CGA CTA GCA GAT  1146

    G   S   N   N   C   S   G   R   V   E   V   R   I   H   E   Q   W   W   T   I   393
   GGA AGT AAC AAT TGT TCA GGG AGA GTA GAG GTG AGA ATT CAT GAA CAG TGG TGG ACA ATA  1206

    C   D   Q   N   W   K   N   E   Q   A   L   V   V   C   K   Q   L   G   C   P   413
   TGT GAC CAG AAC TGG AAG AAT GAA CAA GCC CTT GTG GTT TGT AAG CAG CTA GGA TGT CCG  1266

    F   S   V   F   G   S   R   R   A   K   P   S   N   E   A   R   D   I   W   I   433
   TTC AGC GTC TTT GGC AGT CGT CGT GCT AAA CCT AGT AAT GAA GCT AGA GAC ATT TGG ATA  1326

    N   S   I   S   C   T   G   N   E   S   A   L   W   D   C   T   Y   D   G   K   453
   AAC AGC ATA TCT TGC ACT GGG AAT GAG TCA GCT CTC TGG GAC TGC ACA TAT GAT GGA AAA  1386

    A   K   R   T   C   F   R   R   S   D   A   G   V   I   C   S   D   K   A   D   473
   GCA AAG CGA ACA TGC TTC CGA AGA TCA GAT GCT GGA GTA ATT TGT TCT GAT AAG GCA GAT  1446

    L   D   L   R   L   V   G   A   H   S   P   C   Y   G   R   L   E   V   K   Y   493
   CTG GAC CTA AGG CTT GTC GGG GCT CAT AGC CCC TGT TAT GGG AGA TTG GAG GTG AAA TAC  1506

    Q   G   E   W   G   T   V   C   H   D   R   W   S   T   R   N   A   A   V   V   513
   CAA GGA GAG TGG GGG ACT GTG TGT CAT GAC AGA TGG AGC ACA AGG AAT GCA GCT GTT GTG  1566

    C   K   Q   L   G   C   G   K   P   M   H   V   F   G   M   T   Y   F   K   E   533
   TGT AAA CAA TTG GGA TGT GGA AAG CCT ATG CAT GTG TTT GGT ATG ACC TAT TTT AAA GAA  1626

    A   S   G   P   I   W   L   D   D   V   S   C   I   G   N   E   S   N   I   W   553
   GCA TCA GGA CCT ATT TGG CTG GAT GAC GTT TCT TGC ATT GGA AAT GAG TCA AAT ATC TGG  1686

    D   C   E   H   S   G   W   G   K   H   N   C   V   H   R   E   D   V   I   V   573
   GAC TGT GAA CAC AGT GGA TGG GGA AAG CAT AAT TGT GTA CAC AGA GAG GAT GTG ATT GTA  1746

    T   C   S   G   D   A   T   W   G   L   R   L   V   G   G   S   N   R   C   S   593
   ACC TGC TCA GGT GAT GCA ACA TGG GGC CTG AGG CTG GTG GGC GGC AGC AAC CGC TGC TCG  1806

    G   R   L   E   V   Y   F   Q   G   R   W   G   T   V   C   D   D   G   W   N   613
   GGA AGA CTG GAG GTG TAC TTT CAA GGA CGG TGG GGC ACA GTG TGT GAT GAC GGC TGG AAC  1866

    S   K   A   A   A   V   V   C   S   Q   L   D   C   P   S   S   I   I   G   M   633
   AGT AAA GCT GCA GCT GTG GTG TGT AGC CAG CTG GAC TGC CCA TCT TCT ATC ATT GGC ATG  1926

    G   L   G   N   A   S   T   G   Y   G   K   I   W   L   D   D   V   S   C   D   653
   GGT CTG GGA AAC GCT TCT ACA GGA TAT GGA AAA ATT TGG CTC GAT GAT GTT TCC TGT GAT  1986

    G   D   E   S   D   L   W   S   C   R   N   S   G   W   G   N   N   D   C   S   673
   GGA GAT GAG TCA GAT CTC TGG TCA TGC AGG AAC AGT GGG TGG GGA AAT AAT GAC TGC AGT  2046

    H   S   E   D   V   G   V   I   C   S   D   A   S   D   M   E   L   R   L   V   693
   CAC AGT GAA GAT GTT GGA GTG ATC TGT TCT GAT GCA TCG GAT ATG GAG CTG AGG CTT GTG  2106

    G   G   -S  S   R   C   A   G   K   V   E   V   N   V   Q   G   A   V   G   I   713
   GGT GGA AGC AGC AGG TGT GCT GGA AAA GTT GAG GTG AAT GTC CAG GGT GCC GTG GGA ATT  2166

    L   C   A   N   G   W   G   M   N   I   A   E   V   V   C   R   Q   L   E   C   733
   CTG TGT GCT AAT GGC TGG GGA ATG AAC ATT GCT GAA GTT GTT TGC AGG CAA CTT GAA TGT  2226
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      G   S   A   I   R   V   S   R   E   P   H   F   T   E   R   T   L   H   I   L    753
     GGG TCT GCA ATC AGG GTC TCC AGA GAG CCT CAT TTC ACA GAA AGA ACA TTA CAC ATC TTA  2286

      M   S   N   S   G   C   T   G   G   E   A   S   L   W   D   C   I   R   W   E    773
     ATG TCG AAT TCT GGC TGC ACT GGA GGG GAA GCC TCT CTC TGG GAT TGT ATA CGA TGG GAG  2346

      W   K   Q   T   A   C   H   L   N   M   E   A   S   L   I   C   S   A   H   R    793
     TGG AAA CAG ACT GCG TGT CAT TTA AAT ATG GAA GCA AGT TTG ATC TGC TCA GCC CAC AGG  2406

      Q   P   R   L   V   G   A   D   M   P   C   S   G   R   V   E   V   K   H   A    813
     CAG CCC AGG CTG GTT GGA GCT GAT ATG CCC TGC TCT GGA CGT GTT GAA GTG AAA CAT GCA  2466

      D   T   W   R   S   V   C   D   S   D   F   S   L   H   A   A   N   V   L   C    833
     GAC ACA TGG CGC TCT GTC TGT GAT TCT GAT TTC TCT CTT CAT GCT GCC AAT GTG CTG TGC  2526

      R   E   L   N   C   G   D   A   I   S   L   S   V   G   D   H   F   G   K   G    853
     AGA GAA TTA AAT TGT GGA GAT GCC ATA TCT CTT TCT GTG GGA GAT CAC TTT GGA AAA GGG  2586

      N   G   L   T   W   A   E   K   F   Q   C   E   G   S   E   T   H   L   A   L    873
     AAT GGT CTA ACT TGG GCC GAA AAG TTC CAG TGT GAA GGG AGT GAA ACT CAC CTT GCA TTA  2646

      C   P   I   V   Q   H   P   E   D   T   C   I   H   S   R   E   V   G   V   V    893
     TGC CCC ATT GTT CAA CAT CCG GAA GAC ACT TGT ATC CAC AGC AGA GAA GTT GGA GTT GTC  2706

      C   S   R   Y   T   D   V   R   L   V   N   G   K   S   Q   C   D   G   Q   V    913
     TGT TCC CGA TAT ACA GAT GTC CGA CTT GTG AAT GGC AAA TCC CAG TGT GAC GGG CAA GTG  2766

      E   I   N   V   L   G   H   W   G   S   L   C   D   T   H   W   D   P   E   D    933
     GAG ATC AAC GTG CTT GGA CAC TGG GGC TCA CTG TGT GAC ACC CAC TGG GAC CCA GAA GAT  2826

      A   R   V   L   C   R   Q   L   S   C   G   T   A   L   S   T   T   G   G   K    953
     GCC CGT GTT CTA TGC AGA CAG CTC AGC TGT GGG ACT GCT CTC TCA ACC ACA GGA GGA AAA  2886

      Y   I   G   E   R   S   V   R   V   W   G   H   R   F   H   C   L   G   N   E    973
     TAT ATT GGA GAA AGA AGT GTT CGT GTG TGG GGA CAC AGG TTT CAT TGC TTA GGG AAT GAG  2946

      S   L   L   D   N   C   Q   M   T   V   L   G   A   P   P   C   I   H   G   N    993
     TCA CTT CTG GAT AAC TGT CAA ATG ACA GTT CTT GGA GCA CCT CCC TGT ATC CAT GGA AAT  3006

      T   V   S   V   I   C   T   G   S   L   T   Q   P   L   F   P   C   L   A   N   1013
     ACT GTC TCT GTG ATC TGC ACA GGA AGC CTG ACC CAG CCA CTG TTT CCA TGC CTC GCA AAT  3066

      V   S   D   P   Y   L   S   A   V   P   E   G   S   A   L   I   C   L   E   D   1033
     GTA TCT GAC CCA TAT TTG TCT GCA GTT CCA GAG GGC AGT GCT TTG ATC TGC TTA GAG GAC  3126

      K   R   L   R   L   V   D   G   D   S   R   C   A   G   R   V   E   I   Y   H   1053
     AAA CGG CTC CGC CTA GTG GAT GGG GAC AGC CGC TGT GCC GGG AGA GTA GAG ATC TAT CAC  3186

      D   G   F   W   G   T   I   C   D   D   G   W   D   L   S   D   A   H   V   V   1073
     GAC GGC TTC TGG GGC ACC ATC TGT GAT GAC GGC TGG GAC CTG AGC GAT GCC CAC GTG GTG  3246

      C   Q   K   L   G   C   G   V   A   F   N   A   T   V   S   A   H   F   G   E   1093
     TGT CAA AAG CTG GGC TGT GGA GTG GCC TTC AAT GCC ACG GTC TCT GCT CAC TTT GGG GAG  3306

      G   S   G   P   I   W   L   D   D   L   N   C   T   G   T   E   S   H   L   W   1113
     GGG TCA GGG CCC ATC TGG CTG GAT GAC CTG AAC TGC ACA GGA ACG GAG TCC CAC TTG TGG  3366
```

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  Q   C   P   S   R   G   W   G   Q   H   D   C   R   H   K   E   D   A   G   V   1133
 CAG TGC CCT TCC CGC GGC TGG GGG CAG CAC GAC TGC AGG CAC AAG GAG GAC GCA GGG GTC  3426

  I   C   S   E   F   T   A   L   R   L   Y   S   E   T   E   T   E   S   C   A   1153
 ATC TGC TCA GAA TTC ACA GCC TTG AGG CTC TAC AGT GAA ACT GAA ACA GAG AGC TGT GCT  3486

  G   R   L   E   V   F   Y   N   G   T   W   G   S   V   G   R   R   N   I   T   1173
 GGG AGA TTG GAA GTC TTC TAT AAC GGG ACC TGG GGC AGC GTC GGC AGG AGG AAC ATC ACC  3546

  T   A   I   A   G   I   V   C   R   Q   L   G   C   G   E   N   G   V   V   S   1193
 ACA GCC ATA GCA GGC ATT GTG TGC AGG CAG CTG GGC TGT GGG GAG AAT GGA GTT GTC AGC  3606

  L   A   P   L   S   K   T   G   S   G   F   M   W   V   D   D   I   Q   C   P   1213
 CTC GCC CCT TTA TCT AAG ACA GGC TCT GGT TTC ATG TGG GTG GAT GAC ATT CAG TGT CCT  3666

  K   T   H   I   S   I   W   Q   C   L   S   A   P   W   E   R   R   I   S   S   1233
 AAA ACG CAT ATC TCC ATA TGG CAG TGC CTG TCT GCC CCA TGG GAG CGA AGA ATC TCC AGC  3726

  P   A   E   E   T   W   I   T   C   E   D   R   I   R   V   R   G   G   D   T   1253
 CCA GCA GAA GAG ACC TGG ATC ACA TGT GAA GAT AGA ATA AGA GTG CGT GGA GGA GAC ACC  3786

  E   C   S   G   R   V   E   I   W   H   A   G   S   W   G   T   V   C   D   D   1273
 GAG TGC TCT GGG AGA GTG GAG ATC TGG CAC GCA GGC TCC TGG GGC ACA GTG TGT GAT GAC  3846

  S   W   D   L   A   E   A   E   V   V   C   Q   Q   L   G   C   G   S   A   L   1293
 TCC TGG GAC CTG GCC GAG GCG GAA GTG GTG TGT CAG CAG CTG GGC TGT GGC TCT GCT CTG  3906

  A   A   L   R   D   A   S   F   G   Q   G   T   G   T   I   W   L   D   D   M   1313
 GCT GCC CTG AGG GAC GCT TCG TTT GGC CAG GGA ACT GGA ACC ATC TGG TTG GAT GAC ATG  3966

  R   C   K   G   N   E   S   F   L   W   D   C   H   A   K   P   W   G   Q   S   1333
 CGG TGC AAA GGA AAT GAG TCA TTT CTA TGG GAC TGT CAC GCC AAA CCC TGG GGA CAG AGT  4026

  D   C   G   H   K   E   D   A   G   V   R   C   S   G   Q   S   L   K   S   L   1353
 GAC TGT GGA CAC AAG GAA GAT GCT GGC GTG AGG TGC TCT GGA CAG TCG CTG AAA TCA CTG  4086

  N   A   S   S   G   H   L   A   L   I   L   S   S   I   F   G   L   L   L   L   1373
 AAT GCC TCC TCA GGT CAT TTA GCA CTT ATT TTA TCC AGT ATC TTT GGG CTC CTT CTC CTG  4146

  V   L   F   I   L   F   L   T   W   C   R   V   Q   K   Q   K   H   L   P   L   1393
 GTT CTG TTT ATT CTA TTT CTC ACG TGG TGC CGA GTT CAG AAA CAA AAA CAT CTG CCC CTC  4206

  R   V   S   T   R   R   R   G   S   L   E   E   N   L   F   H   E   M   E   T   1413
 AGA GTT TCA ACC AGA AGG AGG GGT TCT CTC GAG GAG AAT TTA TTC CAT GAG ATG GAG ACC  4266

  C   L   K   R   E   D   P   H   G   T   R   T   S   D   D   T   P   N   H   G   1433
 TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT  4326

  C   E   D   A   S   D   T   S   L   L   G   V   L   P   A   S   E   A   T   K   1453
 TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA  4386

  *                                                                              1454
 TGA                                                                             4389
```

CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACAACTTTTAAATGAATAAAGAGGA 4468

AGTCAAGTTGCCCTATGGAAAACTTGTCCAAATAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGG 4547

TGATAATAAAAATTGAATTATGTATATCACTGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACGGACGCGTGGGTCG   4626

AC   4628

Fig. 2E

Fig. 2F
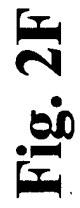
Fig. 2G

```
             10        20        30        40        50        60        70
Hum   MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLLNSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWG
      : :          ::     : .: .      :.::!..   ...   : .:::::: .:   : : ::::: ::.::
WCl   MAL---------GR---HLSLRGL---CVLLLGT--MVG---GQALELRLKDGVHRCEGRVEVKHQGEWG
                           10        20        30        40        50


             80        90       100       110       120       130
Hum   TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH---REWGSHN
      ::  .   :.   ..::::!!:  ... :    : :::  .:: .:. ...: ...:    .. ...:
WCl   TVDGYRWTLKDASVVCRQLGCGAAIG-FPGGAYFGPGLGPIWLLYTSCEGTESTVSDCEHSNIKDYRNDG
                 60        70        80        90       100       110


      140       150       160       170       180       190       200
Hum   CYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSG
      ::  :.:: :  :      .::.::..:!::::::   : :  :: :.:v  ..:  ..: .::  .       :
WCl   YNHGRDAGVVCSG----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG
      120       130       140       150       160       170       180


      210       220       230       240       250       260       270
Hum   VVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVE
       .  ..:  ...  :.:.: .::  : .     .  : .  .. ... :  ... :   ...:.::  : .::
WCl   HELFRESSAQVWAEEFRCEGEEPELWVCPRVPCPGGTCHHSGSAQVVCSAYSEVRL-MTNGSSQCEGQVE
      190       200       210       220       230       240       250


      280       290       300       310       320       330       340
Hum   LKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGT
      ..: :.: ..:       :. :.:.:.:..:!:::!.:  .: ::     .:  .   :::.:.:::.:   ..
WCl   MNISGQWRALCASHWSLANANVICRQLGCGVAISTPGGPHLVEEGDQILTARFHCSGAESFLWSCPVTAL
      260       270       280       290       300       310       320


      350       360       370       380       390       400       410
Hum   VNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSV
      . ::  : :  .:!:::: :....                                    :.:   :...       ::
WCl   GGPDCSHGNTASVICS-GNQI-------------------------------------QVLPQCND-----SV
      330       340                                              350


      420       430       440       450       460       470       480
Hum   FGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY
       ..:.. :           ....::        :                        ::: .:  :::!.. .:!
WCl   -----SQPTGSA----------ASEDSA----PY---------------CSDSRQL--RLVDGGGPCA
            360                                         370       380


      490       500       510       520       530       540       550
Hum   GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
      ::.:.  :: ::   :: ::.::..:. : :::::::.:.... : : .. ..:::!:!.:!:!.:::!.: :
WCl   GRVEILDQGSWGTICDDGWDLDDARVVCRQLGCGEALNATGSAHFGAGSPIWLDNLNCTGKESHVWRCP
      390       400       410       420       430       440       450
```

```
          560        570        580        590        600        610        620
Hum  HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDC
     ::::::::  :..:.:  :.:    ..::.:. ..:.:..:..:: ::..::.  ::: ::: ..:
WCl  SRGWGQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGSVCRNPMEDITVSTICRQLGC
          460        470        480        490        500        510        520


          630        640        650        660        670        680        690
Hum  PSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGS
     .:  ..:        ::.     :.:.:  :.:.::  :: :::: .::.  .::::. ..:::::.
WCl  GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSLWQCPSDPWNYNSCSPKEEAYIWCADSR--QIRLVDGG
          530        540        550        560        570        580        590


          700        710        720        730        740        750        760
Hum  SRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL
     .::.:.::.   ::  ..:.. .:...  :  ::::.::.  ::  ::.::. .:.:. .:.:: .. .
WCl  GRCSGRVEILDQGSWGTICDDRWDLDDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV
          600        610        620        630        640        650        660


          770        780        790        800        810        820        830
Hum  WDCIRWEWKQTACHLNMEASLICSAHRQPRLVGAEMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL
     : :  :  :.: ..: ..:..::.       :::..: ::::::::: ...: :: :..:.: ..:..: ::
WCl  WRCPSWGWRQHNCNHQEDAGVICSGF--VRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL
          670        680        690        700        710        720        730


          840        850        860        870        880        890        900
Hum  NCGDAISLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLV-NG
     .::  :.:.      :     ..:  .::: :.:.:.:   :  :  :.  :.  .:: ::..:.:. ::
WCl  GCGKAVSVLGHMPFRESDGQVWAEEFRCDGGEPELWSCPRVPCPGGTCLHSGAAQVVCSVYTEVQLMKNG
          740        750        760        770        780        790        800


          910        920        930        940        950        960        970
Hum  KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESL
     ::::.::::.:.  ..: :.:  .::...:. :.:::::.:.:: :.  : :  . :  .::: :.::.
WCl  TSQCEGQVEMKISGRWRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF
          810        820        830        840        850        860        870


          980        990        1000       1010       1020       1030       1040
Hum  LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC
     .: .:..:.::.:  : ::::::.:::.::: :.  :  .:.  ::..: :. :. : ..:::::::... :
WCl  LWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAASEESSPYCSDSRQLRLVDGGGPC
          880        890        900        910        920        930        940


          1050       1060       1070       1080       1090       1100       1110
Hum  AGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQC
     .:::::  ...   :::::::.::::::.:::::::::.::::::::.::::::::::::::::. :: :: :
WCl  GGRVEILDQGSWGTICDDDWDLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDDLNCTGKESHVWRC
          950        960        970        980        990        1000       1010


          1120       1130       1140       1150       1160       1170       1180
Hum  PSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLG
     ::::::::::.::::::::::::: :::. ::  ::   :::::::::::::::: ::.  .  .:...:::::
WCl  PSRGWGRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG
          1020       1030       1040       1050       1060       1070
```

Fig. 2H

```
         1190      1200      1210      1220      1230      1240
Hum CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDR----------
    ::..:  .. .  .  :: .   ::: :::: ..:.:::  :.::    :: ::. :..:.:
WCl CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSGPWKYSSCSPKEEAYISCEGRRPKSCPTAAA
       1080      1090      1100      1110      1120      1130      1140


            1250      1260      1270      1280      1290      1300
Hum  ------IRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIW
           .:.::::.::::::::::::. ::::::::::::. ::.:.:.::.::.:
WCl CTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDDSWSLAEAEVVCQQLGCGQALEAVRSAAFGPGNGSIW
       1150      1160      1170      1180      1190      1200      1210


     1310      1320      1330      1340                  1350      1360
Hum  LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG---------------QSLKSLNASSGHLALI
     ::..:  :  ::  ::::  :  ::::::::. : :::::::::::      .:  .. ..:  :  ::
WCl  LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNSLPGIFSLPGVLCLI
       1220      1230      1240      1250      1260      1270      1280


         1370      1380          1390          1400          1410
Hum  LSSIFGLLLLVLFILFLTWCRVQK------QKHLPLRVS-------TRRRG--------SLEENLFHEME
     :..:..  :.:.:.. ..: :  :...   .  :.  :       :... :       .. ..   :  :
WCl  LGSLLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
       1290      1300      1310      1320      1330      1340      1350


                  1420                1430                1440
Hum  TC---------------LKREDPHGTRTSD--------DTPNHGCEDAS------------DTSLLGV
        . :   .:.:.:.         ...: : ..:            :     :..
WCl  EVPVPGTPSPSQGNEEEVPPPEKEDGVRSSQTGSFLNFSREAANPGEGEESFWLLQGKKGDAGYDDVELSA
       1360      1370      1380      1390      1400      1410      1420


        1450
Hum  LPASEAT-K
     :  .: .:
WCl  LGTSPVTFS
       1430
```

Fig. 2I

Fig. 2J

```
              10        20        30        40        50        60        70
Hum  ATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGAACCTTTTCTCTG
     :::          .::: :::                          ::.:.::      ::: : : :::
WCl  ATG-------------GCTC-TGG---------------------GCAGACA------CCTCT-CCCTG
                       10                                       20


              80        90       100       110       120       130       140
Hum  CTGTGGTAACTTGCATCCTGCTCCTGAATTCCTGCTTTCTCATCAGCAGTTTTAATGGAACAGATTTGGA
     : ::..  :  .:::: ::::: :       : ::.     :        ::  : ..:::.  :: : .:::
WCl  C-GGGGACTCT-GTGTCCTCCTCCT------CGGCA----C-----CATGGTGGGTGGTCAAGCTCTGGA
        30        40        50                       60        70        80


             150       160       170       180       190       200       210
Hum  GTTGAGGCTGGTCAATGGAGACGGTCCCTGCTCTGGGACAGTGGAGGTGAAATTCCAGGGACAGTGGGGG
     : ::::: ::.. .:::::::.: .:: :::     :::: :::::::::: .:::::: :.::::: :
WCl  GCTGAGGTTGAAGGATGGAGTCCATCGCTGTGAGGGGAGAGTGGAAGTGAAGCACCAAGGAGAATGGGGC
              90       100       110       120       130       140       150


             220       230       240       250       260       270
Hum  ACTGTGTGTGATGATGGGTGGAACACTACTGCCT-CAACTGTCGTGTGCAAACAGCTTGGATGTCCATTT
     ::.::: .:.:.: :  .:::::: :: :. .:   : ::.:::  ::::::::.::::: ::.:::   :  :
WCl  ACAGTGGATGGTTACAGGTGGA-CATTGAAGGATGCATCTGTAGTGTGCAGACAGCTGGGGTGTGGAGCT
              160      170       180       190       200       210


      280       290       300       310       320       330       340
Hum  TCTTTCGCCATGTTTCGTTTTGGACAAGCCGTGA--CTAGACATGGAAAAATTTGGCTTGATGATGTTTC
        : .: :  .: :: :    . ::.:...   ::.  :..:::.::: ::::::::: .  ::. :::
WCl  GCCATTG--GTTTTCCTGGAGGGGCTTATTTTGGGCCAGGACTTGGCCCCATTTGGCTTTTGTATACTTC
     220       230       240       250       260       270       280


      350       360       370       380       390       400       410
Hum  CTGTTATGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAATGGGGAAGCCATAACTGTTATCAT
        ::: :..:.: .:::::::.: ::..: :: ::: :.::       :::.  .::: : :..: :::.:: ::
WCl  ATGTGAAGGGACAGAGTCAACTGTCAGTGACTGTGAGCAT-TCTAATATTAAAGAC-TATC-GTAATGAT
     290       300       310       320       330       340       350


      420       430       440       450       460       470       480
Hum  GGAGAAGATGTTGGTGTGAACTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
     ::  :..  ::  .::::  .:   : :::::.:: :.. ::.:.:.::::.:      ::.: :::: ::..  .
WCl  GGCTATAATCATGGTCGGGA---TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
        360       370          380       390       400       410       420


      490       500       510       520       530       540       550
Hum  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
     .:: ::::: :::::::  :::::.::.::: :.: :..::.:.:      ::..: ..:::: ::::::::.. .
WCl  GAC-CCTGCTCAGGGCGAGTAGAAGTGCATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
        430       440       450       460       470       480
```

```
        560       570       580       590       600       610       620
Hum ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTTATTTCTTCTGGAGTTGT
     .: .  .:: .:::::   :::            :::.::: :        .:.. : :
WCI TCACACTTGCCACTGCC-------CAG--------------ATCATCTGT-------GCAGAGTTGGG
     490       500                              510            520


        630       640       650       660       670       680       690
Hum TAATAGCCCTGCTGTATTGCGCCCCATTTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT-
     :..:.::          ..:::::: ::..: :     :::::.:: ::::    :..::
WCI TTGTGGC-------------------AAGGCTG--TGTCTGT-----CCTGGGACATGAG----CTCTT
     530                        540            550       560


        700       710       720       730       740       750       760
Hum CTGGAATTGCAGACATCGTGGATGGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT
     :.:..:  :  :::. :         ::  :.::: : :      :::.:: :::        :
WCI CAGAGAGTCCAGT-GCC-------------CAGGTCTG--GGC----TGAAGAGTTCA-------GG
     570        580                 590           600


        770       780       790       800       810       820       830
Hum TATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACTAACCGCTGTATGGGGAGAGTAGAGCTGA
     :.:::  .:  ..  ::  :  :  :::.::     ::  :::..:::. :: :.:..::      :::
WCI TGTGAGGGGGAGGAGCCTGAGCT----CT-------GGGTCTGCCC-CAGAGTG---------CCCTG-
     610       620           630            640                 650


        840       850       860       870       880       890       900
Hum AAATCCAAGGAAGGTGGGGGACCGTATGCCACCATAAGTGGAACAATGCTGCAGCTGATGTCGTATGCAA
     :::::      :::::: :::.:  :::::  :  :::::.: ::::  ::: :  .:  :   :  .:::.
WCI ---TCCA--------GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT
                    660       670       680            690       700


        910       920       930       940       950       960       970
Hum GCAGTTGGGATGTGGAACCGCACTTCACTTCGCTGGCTTGCCTCATTTGCAGTCAGGGTCTGATGTTGTA
     .:.       .:..:. :  ::::.:: ::..  .:  :::::     ::::  : .:  .:: :.:.:: .:..
WCI ACT------CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT
             710       720       730            740           750       760


        980       990       1000      1010      1020      1030      1040
Hum TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTTCTTTGGGACTGCAGACATTCCGGAACCGTCA
     ..::.:         :::            .:.   ::..:  . :::  : : :       ::::  ::.:.   ::....:: :
WCI GAACATT------TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-ACTGGAGTCTGGCCAATGCC---A
     770           780       790       800       810       820


        1050      1060      1070      1080      1090      1100      1110
Hum ATTTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAACTGCGACT
     ::  :: ..::::::  :::  :.  ..:  .::  .    ::  :::::  :.:     ::::         .::  .: ::: :::
WCI ATGTTATCTGTCGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCCGGAG---------GACCAC-ACT
     830       840       850       860       870              880


        1120      1130      1140      1150      1160      1170      1180
Hum AGCAGATGGAAGTAACAATTGTTCAGGGAGAGTAGAGGTGAGAATTCA-TGAACAGTGGTGGACAATATG
     .:   .::::::::.   ::.::::   :   :: .: :    :::::::  :::   :   :::.:  ::
WCI TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCGATTTCACTGCTCTG----GGGC----TG
        890       900       910       920       930
```

<div style="text-align:center">

Fig. 2K

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```
          1190      1200      1210      1220      1230      1240      1250
Hum  TGACCAGAACTGGAAGAATGAACAAGCCCTTGTGGTTTGTAAGCAGCTAGGATGTCCGTTCAGCGTCTTT
     .:.::. . :::  .....::.       ::: :::. :     ::  ::.:::. :::: ..:.:   : .:
WCI  AGTCCT-TCCTGTGGAGTTGT------CCT-GTGACT-----GCC-CTGGGTGGTCCTGACTGTTCCCAT
     940       950       960             970       980       990


          1260      1270      1280      1290      1300      1310      1320
Hum  GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGG
     :::. .  .:. :.  ..: ::. : ::::.: ::: .:: :  ::: . .:  . :.: :
WCI  GGCAACACAGCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCAGTGCAACGA-CTCCG--
         1000      1010      1020      1030      1040      1050      1060


          1330      1340      1350      1360      1370      1380      1390
Hum  AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATG
     ::. :::.. ..:.:: .::::    ::      :. :: :.:::: .: ::        :... ::
WCI  --TGTCTCAACCTACAGGCTCTGC---------GGC----CTCAGAGGACA-GCGCCC-----CCTACTG
           1070      1080                   1090      1100


          1400      1410      1420      1430      1440      1450      1460
Hum  CTGGAGTAATTTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCATAGCCCCTGTTATGG
     ::  ...      :.:   ::::::: :: :  ::::.. :  :.::::: :   .: ::::: ::
WCI  CTCAGA---------CAG--CAGGCAGCTCCG--CCTGGTG---GACGGGG-GC--GGTCCCTGCGCCGG
     1110                1120      1130              1140      1150      1160


          1470      1480      1490      1500      1510      1520
Hum  GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTCATGACAGATGGAGCACAAGG-AATGC
     ::::: :::::.:  ..  :::::.:: :::::  :: .: ::: :::::.: :::..: ::..:. .:::
WCI  GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC
         1170      1180      1190      1200      1210      1220


     1530      1540      1550      1560      1570      1580      1590
Hum  A-GCTGTTGTGTGTAAACAATTGGGATGTGGA-AAGCCTATGCATGTGTTTGGTATGACCTATTTTAAAG
     :: ::  :::::: :...:. :::: ::::::  ::::: . . .::  .  :: .  .: .: : :: ...:
WCI  CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG
     1230      1240      1250      1260      1270      1280      1290


     1600      1610      1620      1630      1640      1650      1660
Hum  AAGCATCAGGACCTATTTGGCTGGATGACGTTTCTTGCATTGGAAATGAGTCAAATATCTGGGACTGTGA
      :: ::::::.:: :: ::: :::: ::::  .:: :   :::: .::::: .::::: : .: ::... ::
WCI  CAGGATCAGGGCCCATCTGGTTGGACAACTTGAACTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCCC
     1300      1310      1320      1330      1340      1350      1360


     1670      1680      1690      1700      1710      1720      1730
Hum  ACACAGTGGATGGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA
     .  : : :: :::::.. :::: :: :: . :::::.. :::: : :.  :: : :::::::: ..: :
WCI  TTCCCGGGGCTGGGGGGCAGCACAACTGCAGACACAAGCAGGACGCGGGGGTCATCTGCTCAG--AGTTC-
     1370      1380      1390      1400      1410      1420      1430


     1740      1750      1760      1770      1780      1790      1800
Hum  ACATGGGGCCTGAGGCTGGTGGGCGGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC
     :..  :: :::::.  .::  : ::: :::.:. :: :..::.  :.:..::..::.. .:.:  ..::..
WCI  -CT--GGCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGCTGGGTGGCTGGAAGTTTTCTACAATGGGA
         1440      1450      1460      1470      1480      1490      1500
```

Fig. 2L

```
              1810       1820       1830       1840       1850       1860       1870
Hum   GGTGGGGCACAGTGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTGTAGCCAGCTGGACTG
              :::::::: .:: ::   ..:.:: :. :.: .. :. .::: : . :.: :: ::  ::::: :..:::
WCl   CCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
              1510       1520       1530       1540       1550       1560       1570


              1880       1890       1900       1910       1920       1930       1940
Hum   CCCATCTTCTATCATTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAAAAATTTGGCTCGATG
              .    .:..: .. .: .. :::    :::.: ::: :  . :::.::..:. : .::: :. : :::
WCl   T--GGGGACAGTGGAACCCTCAACTCTTCTGTTGCTCTTAGAGAAGGTTTTAGGCCACAGTGGGTGGAT-
                1580       1590       1600       1610       1620      1630


              1950       1960       1970       1980       1990       2000       2010
Hum   ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTG--GGGAAATAATGAC
              .:..::::::.  :::. .:.:  :: ::::: :. :::: ..: :  :. :..::: :  :..: .::
WCl   -AGAATCCAGTGTCGGAAAACTGACACCTCTCT---CTGGCAGTGTCCTTCTGACCCTTGGAATTACAAC
              1640    .  1650       1660       1670       1680       1690       1700


              2020       2030       2040       2050       2060       2070       2080
Hum   TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG
              : ::   :.:.  .:::.:.. ..:  :. :::::  :: .: :::.. :  :  :: : :   :: :::::.
WCl   T-CATGCTCTCCAAAGGAGGAAGCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA
              1710       1720       1730       1740       1750       1760


              2090       2100       2110       2120       2130       2140       2150
Hum   TGGAAGCAGCAGGTGTGCTGGAAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT
              :::::.: .:  :  :: :::::.:.:: :::.: :::::.:.::::::: :: ::: :  :  :::: :.:
WCl   TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGAC
              1770       1780       1790       1800       1810       1820       1830


              2160       2170       2180       2190       2200       2210     .2220
Hum   GGCTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA
              :::::::. ::.::..::  ..:: :: :::::.::.::.:: :. ::::::. ..::   : ::.: :::
WCl   CGCTGGGACCTGGACGATGCCCGTGTGGTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA
             1840       1850       1860       1870       1880       1890       1900


              2230       2240       2250       2260       2270       2280
Hum   GAGA-GCCTCATTTCACAGAA--AGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGA
              .:.  : :: ::  .:.:.:  .::.:: .: :::::: . ::  .:.   ..:::::: ..:::::.:::
WCl   CTGTCTCTTCCTTCTTCGGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGAACTGCAGAGGAGAGGA
              1910       1920       1930       1940       1950       1960       1970


            2290       2300       2310 ⎺  2320       2330       2340       2350
Hum   AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCATTTAAATATGGAAGCAAG
              . ::  . : :::.. ::  .    ::::..::: ..:. :: :: .. :.....::.:.:.:
WCl   GTCCCAAGTATGGAGGTGCCCTTCCTGGGGATGGCGGCAACACAAC-TGCAATCATCAAGAAGATGCAGG
            1980       1990       2000       2010       2020       2030       2040


            2360       2370       2380       2390       2400       2410       2420
Hum   TTTGATCTGCTCAGCCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAA
              . : :::::::::: .::.   :   :::::::::: .... .:.:. .:.:::::::::::::::..::
WCl   AGTCATCTGCTCAGGATTTGTGC------GTCTGGCTGGAGGAGATGGACCCTGCTCAGGGCGAGTAGAA
            2050       2060             2070       2080       2090       2100
```

<div align="center">

Fig. 2M

</div>

```
              2430      2440      2450      2460      2470      2480      2490
Hum   GTGAAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGATTTCTCTCTTCATGCTGCCAATGT--GCT
      ::: :.    :: :::  .: :::   :  :.::  :  : ::::    ..: :::.:.:: :  .:::::  : ::   ::
WCl   GTGCATTCTGGAGAAGCCTGGACCCCAGTGTCTGATGGAAACTTCACACTCCCCACTGCCCAGGTCATCT
        2110      2120      2130      2140      2150      2160      2170


              2500      2510      2520      2530      2540      2550      2560
Hum   GTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGG-AATGG
      .::::::::  :.....::::: .:  ::  .:.:.::  :  :  ::: :.  :  : ::   :.:: ..:.::  .:::::
WCl   GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCTGGGACACATGCCATTCAGAGAGTCCGATGG
        2180      2190      2200      2210      2220      2230      2240


              2570      2580      2590      2600      2610      2620      2630
Hum   TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAA
      :....  :::::  .:::::::.:::::::  .::::: ::  : :: .:  : ::::::.:: .:: :
WCl   CCAGGTCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGGAGCCTGAGCTCTGGTCCTGCCCCAGAGTGCCC
        2250      2260      2270      2280      2290      2300      2310


              2640      2650      2660      2670      2680      2690      2700
Hum   CATCCGGAAGACACTTGTATCCACAGCAGAGAAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGAC
      .::::.:..::..:: ::::::: :::::::   .::: .: :  ..:::::::.: ::  .:: :::::::...:
WCl   TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTACACAGAAGTCCAGC
        2320      2330      2340      2350      2360      2370      2380


              2710      2720           2730      2740      2750      2760      2770
Hum   TTGTGAATGGCAAATCC---CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC
      ::.::::::..  .::    ::.:::::  :::::::.:::::::.: :. ::  :::::.  :::.:  ..:
WCl   TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC
        2390      2400      2410      2420      2430      2440      2450


              2780      2790      2800      2810      2820      2830      2840
Hum   TGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTGTGGGACTGCTCT
      :  :::::  :..::::::::..  :  .:  .::::: .::::  :  ::  :.:::::::.::::::::..  ::  :
WCl   TCTGTGCCTCCCACTGGAGTCTGGCCAATGCCAATGTTGTCTGTCGTCAGCTCGGCTGTGGAGTCGCCAT
        2460      2470      2480      2490      2500      2510      2520


              2850      2860      2870      2880      2890      2900      2910
Hum   CTCAACCACAGGAGGAAAATATATTGGAGAAAGAAGTGTTCGTGTGTGGGGACACAGGTTTCATTGCTTA
      :::: :::   : .::::::  :  : .: : .:::.::.::..::.::  .: :  .. :   :  ..::::: ::::: :
WCl   CTCCACCCCCAGAGGACCACACTTGGTGGAAGGAGGTGATCAGATCTCAACAGCCCAATTTCACTGCTCA
        2530      2540      2550      2560      2570      2580      2590


              2920      2930      2940      2950      2960      2970      2980
Hum   GGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA
      :::. :::::::  : ::: . :. :::: ..:::::.:    : ::.: .::: ::::. :::::: :: :
WCl   GGGGCTGAGTCCTTCCTGTGGAGTTGTCCTGTGACTGCCTTGGGTGGGCCTGACTGTTCCCATGGCAACA
        2600      2610      2620      2630      2640      2650      2660


              2990      3000      3010      3020      3030      3040      3050
Hum   CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCC
      :.: :::::::::::::::::.:::::::.:: :::::: .::::: .:::: : .:::.::: ..  :.::: : ::
WCl   CAGCCTCTGTGATCTGCTCAGGAAACCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACC
        2670      2680      2690      2700      2710      2720      2730
```

Fig. 2N

```
            3060      3070      3080      3090      3100      3110      3120
Hum : ATATTTGTCTGCAGTTCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGAT
       . .  ::::::.:   ::::::::. ::: ::   ..:::::.:::  ..::...:.::::::::::.::::
WCl : TGCAGGCTCTGCGGCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCAGCTCCGCCTGGTGGAC
            2740      2750      2760      2770      2780      2790      2800


            3130      3140      3150      3160      3170      3180      3190
Hum : GGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG
       ::::..::  :::::::::::::::::  :: :: :::: ::::::::::::::::::::::::::::: :
WCl : GGGGGCGGTCCCTGCGGCGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGATG
            2810      2820      2830      2840      2850      2860      2870


            3200      3210      3220      3230      3240      3250      3260
Hum : GCTGGGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT
       .:::::::::.::::::::.:::::::::::::: ..  :::::::::::::::::::::  :::::::::::
WCl : ACTGGGACCTGGACGATGCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCAATGCCACGGG
            2880      2890      2900      2910      2920      2930      2940


            3270      3280      3290      3300      3310      3320      3330
Hum : CTCTGCTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACTGCACAGGAACGGAGTCC
       :::::::::::::::  ::::  .::.::::::::::::::::::::::::.:::::::::::::::  ::::::
WCl : GTCTGCTCACTTCGGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAACTGCACAGGAAAGGAGTCC
            2950      2960      2970      2980      2990      3000      3010


            3340      3350      3360      3370      3380      3390      3400
Hum : CACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGGCAGCACGACTGCAGGCACAAGGAGGACGCAGGGGTCA
       ::: :::::  .:::::::::::: ::::::::::.::::::::::::::::::::.::::::::: :::::::
WCl : CACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGGCGGCACGACTGCAGACACAAGGAGGACGCCGGGGTCA
            3020      3030      3040      3050      3060      3070      3080


            3410      3420      3430      3440      3450      3460      3470
Hum : TCTGCTCAGAATTCACAGCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
       ::::::::::::.:::   .::: : ::: :    ..::::. :  ...:: .. :: ::::::::::::.. ::::
WCl : TCTGCTCAGAGTTCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA
            3090      3100      3110      3120      3130      3140


            3480      3490      3500      3510      3520      3530      3540
Hum : AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCATTGTG
       .::: ::::: :::::::::::::::::: ::: :: : :::   :::  .  .. :: .: .  :.: ..:
WCl : GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCAGCCCCATGGAAGATATCACTGTGTCCGTGATC
            3150      3160      3170      3180      3190      3200      3210


            3550      3560      3570      3580      3590      3600
Hum : TGCAGGCAGCTGGGCTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCCTTTA--TCT-AAGACAGGCTCTG
       ::::::.:::::  :: :::::::::: :.:::::   .:::. : .:.:: :: :.   ::: :.:. ::: :::.
WCl : TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTTGGTCTCAGGGAAGGTTCTA
            3220      3230      3240      3250      3260      3270      3280


            3610      3620      3630      3640      3650      3660      3670
Hum : GTTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC
       :. :  : :::::::: : :::::::::  :::: : ::: :::   : ::::::::: ::: :::: :::
WCl : GACCCCGGTGGGTAGATTTAATTCAGTGTCGGAAAATGGATACCTCTCTCTGGCAGTGTCCTTCTGGCCC
            3290      3300      3310      3320      3330      3340      3350
```

<div align="center">Fig. 20</div>

```
            3680        3690        3700        3710        3720        3730        3740
Hum    ATGGGAGCGAAGAATCTCCAGCCCAGCAGAAGAGACCTGGATCACATGTGAAGATAGAATA----AGAG-
       :::::.:. . ::.. :: :. :::. ..::.::..:::. :::.:::::::::::...:::: : .::::
WCl    ATGGAAATACAGTTCATGCTCTCCAAAGGAGGAAGCCTACATCTCATGTGAAGGAAGAAGACCCAAGAGC
            3360        3370        3380        3390        3400        3410        3420


                                                                  3750        3760
Hum    --------TGC----------------------------------GTGGAGGAGACACCGAGTGCTCTG
               ::: :                                  : ::::::::::: :::::::::::.:
WCl    TGTCCAACTGCTGCCGCCTGCACAGACAGAGAGAAGCTCCGCCTCAGGGGAGGAGACAGCGAGTGCTCAG
            3430        3440        3450        3460        3470        3480        3490


         3770        3780        3790        3800        3810        3820        3830
Hum    GGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGC
       :: :.:.::.: ::::::. :::::::::::: :::: :::::: :::::::::::::::..::::. :::::
WCl    GGCGGGTGGAGGTGTGGCACAACGGCTCCTGGGGCACCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
            3500        3510        3520        3530        3540        3550        3560


         3840        3850        3860        3870        3880        3890        3900
Hum    GGAAGTGGTGTGTCAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAG
       ::.::.:::::::::::::::::::::::::::::: :: :::: .::: :: :: ::. :.::::::.
WCl    TGAGGTGGTGTGTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGTCTGCAGCATTTGGCCCT
            3570        3580        3590        3600        3610        3620        3630


         3910        3920        3930        3940        3950        3960        3970
Hum    GGAACTGGAACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACG
       :::: :::.: :::::::: :::: :: ..:.::::.::::: . ::::: :: ::.::::::: . :
WCl    GGAAATGGGAGCATCTGGCTGGACGAGGTGCAGTGCGGGGGCCGGGAGTCCTCCCTGTGGGACTGTGTTG
            3640        3650        3660        3670        3680        3690        3700


          3980        3990        4000        4010        4020        4030        4040
Hum    CCAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGG---ACAGTC
       : .:.:::::::::.:::::: :::::: ...::.:::::::::::: :::::::::::::::: : .:.:
WCl    CGGAGCCCTGGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAGGAC
            3710        3720        3730        3740        3750        3760        3770


                  4050        4060                 4070        4080        4090
Hum    G-------CTGAAATCACTGAATG--CCT------CCTCAGGT-CATT---TAGCA-CTTATTTTATCCA
               : . .: :::.: : : ::.         :::::..: :. : :.::: ::: : . .::.
WCl    AACATTGCCCACGACCACAGCAGGGACCAGAACAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT
            3780        3790        3800        3810        3820        3830        3840


              4100        4110        4120                 4130        4140
Hum    G--------TATCTT----TGGGCTC-CTTCTC---CTGGTTCT---------GTTTATTCTATTTCTCA
       :        :. :::     :::: :: ::::::    ::::: ::        : : ::.. :.::::
WCl    GGGGTTCTCTGCCTTATCCTGGGGTCGCTTCTCTTCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA
           3850        3860        3870        3880        3890        3900        3910


              4150        4160        4170                         4180
Hum    CGTGGTG--CCGAGTTCAGAAACAAAAACATCT-------GCCC---CT----CAGAGTTT-------
       .:::.: : :::: :::: ::..:. :: ::        :: : :: :.:.::.:
WCl    GATGGAGAGCAGAGCGCAGAGCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
            3920        3930        3940        3950        3960        3970        3980
```

Fig. 2P

```
              4190          4200          4210          4220
Hum   -------CAAC-----CAGAAGGAGGG---GTTCT-CTCG----AGGAGAATTTATTCCATGA------
             :..:     ::::::::::.::   :  :. : :.   ::..::  : .. ::: :::
WCl   CGATTACCTTCTGACACAGAAGGAAGGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCTGATGAAAAT
      3990      4000      4010      4020      4030      4040      4050


        4230                              4240                      4250
Hum   ---GATGGAG----------------ACCTG-----------CCTC-----------AAGAGAGAGGAC
         ::::..:                  .::::            ::::          :.::::..:: .:
WCl   TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
      4060      4070      4080      4090      4100      4110      4120


      4260      4270               4280                  4290
Hum   CCACATGGGACAAGAAC-------------CTCAGA-TGACAC---CC---------CCAA---------
      :: :: ..:.: .::..::            ::::::: .:.:.:   ::          :::.
WCl   CCCCAGAGAAGGAGGACGGGGTGAGGTCCTCTCAGACAGGCTCTTTCCTGAACTTCTCCAGAGAGGCAGC
      4130      4140      4150      4160      4170      4180      4190


            4300          4310          4320          4330
Hum   ----CCATGGTT--GTGAAGA----TGCTAGCGACAC--------------ATCGCTG--TTGGGAGTT
          ::. :: .  :.:::::    :  ::.:: .:.:              .. :::: :. :..:.:
WCl   TAATCCTGGGGAAGGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
      4200      4210      4220      4230      4240      4250      4260


              4340          4350
Hum   CTT-----------CCTG-------CCTCTGAAGCCACAAAA
      ::             ::::        :: :.:...: .  . .
WCl   GTTGAACTCAGTGCCCTGGGAACATCCCCAGTGACTTTCTCG
      4270      4280      4290      4300
```

Fig. 2Q

Fig. 3A

```
                              M   A   L   P   A   L   G   L   D   P   W   S    12
GTCGACCCACGCGTCCGGTCTGTGGCTGAGC ATG GCC CTC CCA GCC CTG GGC CTG GAC CCC TGG AGC  67

  L   L   G   L   F   L   F   Q   L   L   Q   L   L   L   P   T   T   T   A   G    32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CTG CCG ACG ACG ACC GCG GGG  127

  G   G   G   Q   G   P   M   P   R   V   R   Y   Y   A   G   D   E   R   R   A    52
GGA GGC GGG CAG GGG CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA  187

  L   S   F   F   H   Q   K   G   L   Q   D   F   D   T   L   L   L   S   G   D    72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT  247

  G   N   T   L   Y   V   G   A   R   E   A   I   L   A   L   D   I   Q   D   P    92
GGA AAT ACT CTC TAC GTG GGG GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA  307

  G   V   P   R   L   K   N   M   I   P   W   P   A   S   D   R   K   K   S   E   112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA  367

  C   A   F   K   K   K   S   N   E   T   Q   C   F   N   F   I   R   V   L   V   132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT  427

  S   Y   N   V   T   H   L   Y   T   C   G   T   F   A   F   S   P   A   C   T   152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC  487

  F   I   E   L   Q   D   S   Y   L   L   P   I   S   E   D   K   V   M   E   G   172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA  547

  K   G   Q   S   P   F   D   P   A   H   K   H   T   A   V   L   V   D   G   M   192
AAA GGC CAA AGC CCC TTT GAC CCC GCT CAC AAG CAT ACG GCT GTC TTG GTG GAT GGG ATG  607

  L   Y   S   G   T   M   N   N   F   L   G   S   E   P   I   L   M   R   T   L   212
CTC TAT TCT GGT ACT ATG AAC AAC TTC CTG GGC AGT GAG CCC ATC CTG ATG CGC ACA CTG  667

  G   S   Q   P   V   L   K   T   D   N   F   L   R   W   L   H   H   D   A   S   232
GGA TCC CAG CCT GTC CTC AAG ACC GAC AAC TTC CTC CGC TGG CTG CAT CAT GAC GCC TCC  727

  F   V   A   A   I   P   S   T   Q   V   V   Y   F   F   F   E   E   T   A   S   252
TTT GTG GCA GCC ATC CCT TCG ACC CAG GTC GTC TAC TTC TTC TTC GAG GAG ACA GCC AGC  787

  E   F   D   F   F   E   R   L   H   T   S   R   V   A   R   V   C   K   N   D   272
GAG TTT GAC TTC TTT GAG AGG CTC CAC ACA TCG CGG GTG GCT AGA GTC TGC AAG AAT GAC  847

  V   G   G   E   K   L   L   Q   K   K   W   T   T   F   L   K   A   Q   L   L   292
GTG GGC GGC GAA AAG CTG CTG CAG AAG AAG TGG ACC ACC TTC CTG AAG GCC CAG CTG CTC  907

  C   T   Q   P   G   Q   L   P   F   N   V   I   R   H   A   V   L   L   P   A   312
TGC ACC CAG CCG GGG CAG CTG CCC TTC AAC GTC ATC CGC CAC GCG GTC CTG CTC CCC GCC  967

  D   S   P   T   A   P   H   I   Y   A   V   F   T   S   Q   W   Q   V   G   G   332
GAT TCT CCC ACA GCT CCC CAC ATC TAC GCA GTC TTC ACC TCC CAG TGG CAG GTT GGC GGG 1027

  T   R   S   S   A   V   C   A   F   S   L   L   D   I   E   R   V   F   K   G   352
ACC AGG AGC TCT GCG GTT TGT GCC TTC TCT CTC TTG GAC ATT GAA CGT GTC TTT AAG GGG 1087
```

```
K   Y   K   E   L   N   K   E   T   S   R   W   T   T   Y   R   G   P   E   T   372
AAA TAC AAA GAG TTG AAC AAA GAA ACT TCA CGC TGG ACT ACT TAT AGG GGC CCT GAG ACC  1147

N   P   R   P   G   S   C   S   V   G   P   S   S   D   K   A   L   T   F   M   392
AAC CCC CGG CCA GGC AGT TGC TCA GTG GGC CCC TCC TCT GAT AAG GCC CTG ACC TTC ATG  1207

K   D   H   F   L   M   D   E   Q   V   V   G   T   P   L   L   V   K   S   G   412
AAG GAC CAT TTC CTG ATG GAT GAG CAA GTG GTG GGG ACG CCC CTG CTG GTG AAA TCT GGC  1267

V   E   Y   T   R   L   A   V   E   T   A   Q   G   L   D   G   H   S   H   L   432
GTG GAG TAT ACA CGG CTT GCA GTG GAG ACA GCC CAG GGC CTT GAT GGG CAC AGC CAT CTT  1327

V   M   Y   L   G   T   T   T   G   S   L   H   K   A   V   V   S   G   D   S   452
GTC ATG TAC CTG GGA ACC ACC ACA GGG TCG CTC CAC AAG GCT GTG GTA AGT GGG GAC AGC  1387

S   A   H   L   V   E   E   I   Q   L   F   P   D   P   E   P   V   R   N   L   472
AGT GCT CAT CTG GTG GAA GAG ATT CAG CTG TTC CCT GAC CCT GAA CCT GTT CGC AAC CTG  1447

Q   L   A   P   T   Q   G   A   V   F   V   G   F   S   G   G   V   W   R   V   492
CAG CTG GCC CCC ACC CAG GGT GCA GTG TTT GTA GGC TTC TCA GGA GGT GTC TGG AGG GTG  1507

P   R   A   N   C   S   V   Y   E   S   C   V   D   C   V   L   A   R   D   P   512
CCC CGA GCC AAC TGT AGT GTC TAT GAG AGC TGT GTG GAC TGT GTC CTT GCC CGG GAC CCC  1567

H   C   A   W   D   P   E   S   R   T   C   C   L   L   S   A   P   N   L   N   532
CAC TGT GCC TGG GAC CCT GAG TCC CGA ACC TGT TGC CTC CTG TCT GCC CCC AAC CTG AAC  1627

S   W   K   Q   D   M   E   R   G   N   P   E   W   A   C   A   S   G   P   M   552
TCC TGG AAG CAG GAC ATG GAG CGG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG  1687

S   R   S   L   R   P   Q   S   R   P   Q   I   I   K   E   V   L   A   V   P   572
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC  1747

N   S   I   L   E   L   P   C   P   H   L   S   A   L   A   S   Y   Y   W   S   592
AAC TCC ATC CTG GAG CTC CCC TGC CCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT  1807

H   G   P   A   A   V   P   E   A   S   S   T   V   Y   N   G   S   L   L   L   612
CAT GGC CCA GCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG  1867

I   V   Q   D   G   V   G   G   L   Y   Q   C   W   A   T   E   N   G   F   S   632
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA  1927

Y   P   V   I   S   Y   W   V   D   S   Q   D   Q   T   L   A   L   D   P   E   652
TAC CCT GTG ATC TCC TAC TGG GTG GAC AGC CAG GAC CAG ACC CTG GCC CTG GAT CCT GAA  1987

L   A   G   I   P   R   E   H   V   K   V   P   L   T   R   V   S   G   A   672
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGG GCC  2047

A   L   A   A   Q   Q   S   Y   W   P   H   F   V   T   V   T   V   L   F   A   692
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC ACT GTC CTC TTT GCC  2107

L   V   L   S   G   A   L   I   I   L   V   A   S   P   L   R   A   L   R   A   712
TTA GTG CTT TCA GGA GCC CTC ATC ATC CTC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT  2167

R   G   K   V   Q   G   C   E   T   L   R   P   G   E   K   A   P   L   S   R   732
CGG GGC AAG GTT CAG GGC TGT GAG ACC CTG CGC CCT GGG GAG AAG GCC CCG TTA AGC AGA  2227
```

```
  E   Q   H   L   Q   S   P   K   E   C   R   T   S   A   S   D   V   D   A   D      752
GAG CAA CAC CTC CAG TCT CCC AAG GAA TGC AGG ACC TCT GCC AGT GAT GTG GAC GCT GAC     2287


  N   N   C   L   G   T   E   V   A   *                                             762
AAC AAC TGC CTA GGC ACT GAG GTA GCT TAA                                             2317

ACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGA    2396

TGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG    2475

TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCC    2554

CCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAA    2633

CACAGTGTTTCAAGAGATCCTAAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATC    2712

ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCA    2791

TGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACC    2870

ACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT    2949

TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTC    3028

AGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC    3104
```

Fig. 3D

```
                10        20        30        40        50        60        70
Hum.  MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYYAGDERRALSFFHQKGLQDFDTLLLS
      :::::.::  :.::::: .:.:::. :    .:.: :::::::::.: :::  ::::::::::::.:::::::.
Mur.  MALPSLGQDSWSLLRVFFFQLFLLPSLPPASGTGGQGPMPRVKYHAGDGHRALSFFQQKGLRDFDTLLLS
                10        20        30        40 ·      50      · 60        70

                80        90       100       110       120       130       140
Hum.  GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY
      .:::::::::::.:.:::.:.::::. :::::::::::::.::.::::::::::::::::::::::.::::
Mur.  DDGNTLYVGARETVLALNIQNPGIPRLKNMIPWPASERKKTECAFKKKSNETQCFNFIRVLVSYNATHLY
                80        90       100       110       120       130       140

               150       160       170       180       190       200       210
Hum   TCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMR
      .::::::::::::::::::::.::::.::.::.:.::.::.    .:.:::::::::::::::::::::::::
Mur.  ACGTFAFSPACTFIELQDSLLLPILIDKVMDGKGQSPLTLFTSTQAVLVDGMLYSGTMNNFLGSEPILMR
               150       160       170       180       190       200       210

               220       230       240       250       260       270       280
Hum   TLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ
      :::.:.:::::.:::::::.:::::::::::::::::::::::::::::::. :.::::::.:::::::::::
Mur.  TLGSHPVLKTDIFLRWLHADASFVAAIPSTQVVYFFFEETASEFDFFEELYISRVAQVCKNDVGGEKLLQ
               220       230       240       250       260       270       280

               290       300       310       320       330       340       350
Hum   KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF
      ::::::::::::::.:::::::::.:::::::::::::...::::::::::::::::::::::::::::.:::::
Mur.  KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVF
               290       300       310       320       330       340       350

               360       370       380       390       400       410       420
Hum.  KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV
      ::::::::::::::::::.:.:..:.:::::::.:::::::::::::::::::.::::::::::::::::::::
Mur.  KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLMDEHVVGTPLLVKSGVEYTRLAV
               360       370       380       390       400       410       420

               430       440       450       460       470       480       490
Hum.  ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVW
      :.:.:::: ::.::.:::.:: .:::::.  :::: ::::::: ::.:::::::::.:::::.:::::::..:
Mur.  ESARGLDGSSHVVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLSPDSEPVRNLQLAPAQGAVFAGFSGGIW
               430       440       450       460       470·      480       490

               500       510       520       530       540       550       560
Hum.  RVPRANCSVYESCVDCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQS
      ::::::::::::::::::::::::::::::: : ::... .........::::::::::::: :::.:. : ::
Mur.  RVPRANCSVYESCVDCVLARDPHCAWDPESRLCSLLSGST-KPWKQDMERGNPEWVCTRGPMARSPRRQS
               500       510       520       530       540       550

               570       580       590       600       610       620       630
Hum   RPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG
      ::.::.::.::::::::: ::::::::::: ::: : ..::::.:::::::::::::. ::::::::::::::::
Mur.  PPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLLPQDGVGGLYQCVATENG
          560       570       580       590·      600       610       620

               640       650       660       670       680       690       700
Hum.  FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALI
      .::::::::::::::.::::::::::.::::.::.:::::::::.:.:.:::::::.::::::::.::::.:.:
Mur.  YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLT
          630       640       650       660       670       680       690

               710       720       730       740       750       760
Hum.  ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA
      .::::::.::::::::::::::: .::::::::::::::....:  :::::::::::::::.:::::
Mur.  LLLASPLGALRARGKVQGCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA
          700       710       720       730·      740       750       760
```

Fig. 3E

```
                                    10                      20        30
HuM. GTCG-AC-CC---------------ACG----------CGTCCGGT------CTGTGGCTGAGCATGGC
     ::: :: ::                  ::         :.:: :::        :: .:::::: ::::::
Mur. CTCGGACGCCTGGGTTAGGGGTCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
       10       20        30        40        50        60        70

        40        50        60        70        80        90       100
HuM. CCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTC-AGCTGCT
     ::: :::  :::::::::::: : ::::: :::::: ::::   :::: :::::::::: :::: .:::::
Mur. CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTTCTTCCAACT-CTTCCTGCTGCC
            80       90       100       110       120       130

       110       120       130       140       150       160       170
HuM. GCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGAT
     . .: : :.: . .:  : :::. .:: :: :::::::::::::::::.:::::.:::: ::::.::.::
Mur. ATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGAC
     140      150       160       170       180       190       200

       180       190       200        210       220       230       240
HuM. GAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG
     :....:. :::::  ::  :::::::::::: ::..::.::::::::..:: :::::::: :::::::::::. :
Mur. GGGCACAGGGCCCTCAGCTTCTTCCAACAAAAAGGCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG
     210      220       230       240       250       260       270

       250       260       270       280       290       300       310
HuM. ATGGAAATACTCTCTACGTGGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC
     ::::  ::  :::::::::  ::::::::::::::::::::..::.:  :::::::::::::::::.  ::::::..::::
Mur. ATGGCAACACTCTCTATGTGGGGGGCTCGAGAGACCGTCCTGGCCTTGAATATCCAGAACCCAGGAATCCC
     280      290       300       310       320       330       340

       320        330       340       350       360       370       380
HuM. CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG
     :::::::::::::::::::::  :::::::::::::: ::::::::::  ::::::::::::::::::::::
Mur. AAGGCTAAAGAACATGATACCCTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAG
     350      360       370       380       390       400       410

       390       400       410       420       430       440       450
HuM. AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCT
     ::::::::::::::::::::::::::::: ::.::::::: ::::::::::  :: :: ::::: .:::
Mur. AGCAATGAGACACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTATGCCT
     420      430       440       450       460       470       480

       460       470       480       490       500       510       520
HuM. GCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTC
     : :: :::::: :::::::::::: :::::::::::::::::::: :::::: .::::::::::::::::
Mur. GTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTT
     490      500       510       520       530       540       550

       530       540        550       560       570       580       590
HuM. GGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT
     :...:::::::::::::::: ::::::::::::::::  ::::::: :::::::::::  :::::
Mur. GATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCC-TTTGACCCTGTTCACAAGCACACAAGCTGTCTT
     560      570       580       590       600       610       620

        600       610       620       630       640       650       660
HuM. GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACA
     ::: :::::::::::::::: :::: :: :::::::::::::::::::::: ::::::::::::::::::: :::
Mur. GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCCATCCTGATGCGGACA
     630      640       650       660       670       680       690

        670       680       690       700       710       720       730
HuM. CTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGG
     .:::::::::: ::::: ::::::::: :::::.::::: : :::::::::::     :: :::::::: ::::
Mur. CTGGGATCCCATCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGATGCCTCCTTCGTGG
     700      710       720       730       740       750       760
```

```
           740       750       760       770       780       790       800
Hum.  CAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA
      ::::::: ::.:: :::::::::::::::: :::::::: :::::::::::::::::::::::::::::::::
Mur.  CAGCCATTCCATCCACCCAGGTCGTCTATTTCTTCTTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA
           770       780       790       800       810       820       830

           810       820       830       840       850       860       870
Hum.  GAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAG
      ...::: : : ::: :::::::: .::":::::::: ::::::::::: :::::::::::::::::::::::
Mur.  AGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAG
           840       850       860       870       880       890       900

           880       890       900       910       920       930       940
Hum.  AAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCC
      :::::::::::::::::::: ::.::::: ::::::::::.: ::::::::::::::::: ::::::::::::
Mur.  AAGTGGACCACCTTCCTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCC
           910       920       930       940       950       960       970

           950       960       970       980       990       1000      1010
Hum.  GCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG
      :.:::::::::::::::::::::::::::::::::.:.: : :::.:::::::::::::::: :::::::::
Mur.  GCCACGCGGTCCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTG
           980       990       1000      1010      1020      1030      1040

          1020      1030      1040      1050      1060      1070      1080
Hum.  GCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAG
      ::::::::::::::::::::::::::::.::.:: ::::::::::r:::::. ::::::::::.::.::::::.
Mur.  GCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCGAGTCTTTAAA
          1050      1060      1070      1080      1090      1100      1110

          1090      1100      1110      1120      1130      1140      1150
Hum.  GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC
      :::::.:::::.::: :::::::::.::.:: :: ::::::::: ::::: ::::: :.:::. ::.::::
Mur.  GGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGGCTCAGAGGTCAGCCCGA
          1120      1130      1140      1150      1160      1170      1180

          1160      1170      1180      1190      1200      1210      1220
Hum.  GGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT
      :::::::::::::::: .::::::::::::::::: ::..:: :::::::::::::::::::::::: :::::
Mur.  GGCCAGGCAGTTGCTCCATGGGCCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTTCTGAT
          1190      1200      1210      1220      1230      1240      1250

          1230      1240      1250      1260      1270      1280      1290
Hum.  GGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG
      :::::::::::: ::::::::::::::::::::::::::.: ::: :::::::::::::::::::::.:::::
Mur.  GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG
          1260      1270      1280      1290      1300      1310      1320

          1300      1310      1320      1330      1340      1350      1360
Hum.  ACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACA
      .::::: :.::::::::::::::: .::::::: : ::::::::::::.:::.::::::.:: : :: ::::
Mur.  TCAGCTCGGGGGCCTTGATGGGAGCAGCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCCTGCACA
          1330      1340      1350      1360      1370      1380      1390

          1370      1380      1390      1400      1410      1420      1430
Hum.  AGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACC
      ::::::::::: : .::::::::::::::::: :::: :::::::::::::::::::::.::::::: :::::
Mur.  AGGCTGTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTCAGCTGAGCCCTGACTCTGAGCC
          1400      1410      1420      1430      1440      1450      1460

          1440      1450      1460      1470      1480      1490      1500
Hum.  TGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGG
      ::::::: ::::::::::::::::::::.:::::::::::::::::.:::::::::: :::::.:.:::::.
Mur.  TGTTCGAAACCTGCAGCTGGCCCCCGCCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGA
          1470      1480      1490      1500      1510      1520      1530

          1510      1520      1530      1540      1550      1560      1570
Hum.  GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTG
      :: :::: :.:::::: :: :::::::: :::::::::::::::::::::::::: ::::::: ::::::::
Mur.  GTTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCTCACTGTG
          1540      1550      1560      1570      1580      1590      1600
```

Fig. 3G

```
        1580      1590      1600      1610      1620      1630      1640
Hum.  CCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACAT
      :::::::::::.:: :: ::: .:::: :::::::: : : .::... ::  :::::::::::::
Mur.  .CCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT
       1610      1620      1630      1640      1650      1660      1670

        1650      1660      1670      1680      1690      1700    -  1710
Hum.  GGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC
      :::::::: :: :::::::::::: ::: .:: :::::::::::: .:::::::: :::::: ::::::::: :
Mur.  :GGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCC
       1680      1690      1700      1710      1720      1730      1740

        1720      1730      1740      1750      1760      1770      1780
Hum.  CCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAG
      :: ::: :    :::::::::::::::.:::::::::::::::::::::::::::::: : :: :::::::::
Mur.  CCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCGCTGCCCCCACCTGTCAG
       1750      1760      1770      1780      1790      1800      1810

        1790      1800      1810      1820      1830      1840      1850
Hum.  CCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG
      :' ::::::::::: :  :::::::::::::: ::: . :.:: :::::::::::: : :: ::::::::::::
Mur.  CACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG-
       1820      1830      1840      1850      1860      1870      1880

        1860      1870      1880      1890      1900      1910      1920
Hum.  CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTT
      ::::::::::::::: :. ::::::::::.:: ::::: :::::::.::::  :::.::::::: :::::.
Mur.  CTCCCTCTTGCTGCTGCCGCAGGATGGTGTGTCGGGGGCCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC
       1890      1900      1910      1920      1930      1940      1950

        1930      1940      1950      1960      1970      1980      1990
Hum.  TCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAG
      :::::::::::::.::::::: ::::::.::::::::::::::::::: ::::::: ::::: :::::.:::::.:
Mur.  TCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCTGGCGCTGGACCCTGAGCTGGCGG
       1960      1970      1980      1990      2000      2010      2020

        2000      2010      2020      2030      2040      2050      2060
Hum.  GCATCCCCCGGGAGCATGTGAAGGTCCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCA
      ::.: ::::: ::::.::: ::::::::: ::::::::.::::::::::.::  ::.:: :: :::::::::.
Mur.  GCGTTCCCCGTGAGCGTGTGCAGGTCCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCCAGCG
       2030      2040      2050      2060      2070      2080      2090

        2070      2080      2090      2100      2110      2120      2130
Hum.  GTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATC
      :::::::::::::::: ::: ::: :: :: :::::: : :::.: :::::  .:::: :::: ::
Mur.  GTCCTACTGGCCCCATTTTCTCATCGTTACCGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTC
       2100      2110      2120      2130      2140      2150      2160

        2140      2150      2160      2170      2180      2190      2200
Hum.  CTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTG
      ::: : :: :::::: ::..:::.:: :::::::::: ::::::::::::::::::::::.:: ::::: ::: .
Mur.  CTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGGTTCAGGGCTGTGGGATGCTGCCCCCCA
       2170      2180      2190      2200      2210      2220      2230

        2210      2220      2230      2240      2250      2260      2270
Hum.  .GGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA
      :::::: :::: :: :::::::: :::::::: :::: :::::::::::::::.::::::::::::::::::::
Mur.  GGGAAAAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA
       2240      2250      2260      2270      2280      2290      2300

        2280      2290      2300      2310      2320      2330      2340
Hum.  TGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG---C
      ::.:: :: :::::::::::: ::::::::::.::::: ::::::::::::  .:.:::::: ::: ::::: :
Mur.  .CGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC
       2310      2320      2330      2340      2350      2360      2370

        2350      2360      2370      2380      2390      2400      2410
Hum.  GGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAA
      .:.:::.:: :::::::.:: :::::. :: ::.:::::::   :::: ::..: :.
Mur.  AGAGCAAGCCACTGGCCTTGTTGGCTATGC----CAGGCACAG----------------TGCCACTCT--
       2380      2390      2400      2410                       2420
```

Fig. 3H

```
                2420      2430      2440      2450      2460      2470      2480
Hvm...  AGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC
        :::::            :. :::::      :: :: : :::::.:: .::.:::.:...:::      :
Mur.    -GACCA----------GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-------C
                          2430      2440      2450      2460

                2490      2500      2510.     2520      2530      2540      2550
Hvm.   ACAGCAGTCTG-CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCT
       ::  ::::  :    :::::.:::::::::::::.:  .:::::::.:                 ::::::
Mur..   ACC-CAGTAGGTCCTCCCCTGTGGGACTCTCTTCTGC-AAGCACATT-----------------GGGCT
        2470      2480      2490      2500      2510

                2560      2570      2580      2590      2600      2610
Hvm.   .ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAG
       :..: ::: ::::: :::::: :.:::.: : :::::::.::.:.  :::.: ::: ..:: ::. .. :::.
Mur.   GTCTCCATACCTGTACTTGTGCTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTGATTTTGATTGACCCAA
        2520      2530      2540      2550      2560      2570      2580

       2620      2630      2640      2650      2660      2670      2680
Hva.   GGACCCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAAAAAACCTGCCTGTCCCAGGACCCTATGGTA
       :...:::: ::.:.:::: : ::: : ::.:::: ::...::.. :: ::::: .::: ::.:.:::._
Mur.   GAGCCCTGCCTGTAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG-
        2590      2600      2610      2620      2630      2640      2650

       2690      2700      2710      2720.          2730      2740      2750
Hvm.   ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAAACT-CCACTCTGAA--
       : .::: : ::.:::: .:..::: : ::::.: ::: : :::    ::..: .:::::::: :::......:
Mur.   ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACGCTGTCACTCTAGA
        2660      2670      2680      2690      2700      2710      2720

                2760      2770      2780      2790      2800      2810
Hvm.   ----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC
           :::::  :::::::.::::: .: :.:::: :: :::::.: :::.    .::..:: :: :::: ::
Mur.   AGCAGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT
        2730      2740      2750      2760      2770      2780      2790

       2820      2830      2840      2850      2860      2870      2880
Hvm.   TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGC
       :::: ::::::::: ::    .::: :   .::::::::.: :::::::::::::.:::::::: :::::::
Mur.   TTCCTTTACCAGTCGGGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACCTTCCTTCTTGG
        2800      2810      2820      2830      2840      2850

                2890      2900      2910      2920      2930      2940      2950
Hvm.   TTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTC
       :::::::: ::.:::: :: :::    : ::::::::::::...: :..:: .::::::::::::::::::
Mur.   TTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGAATGGGGGGCATAATCTGAGCCTTGTTC
        2860      2870      2880      2890      2900      2910      2920

                2960      2970      2980      2990      3000      3010
Hvm.   ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCCTTTGTTTTGGGATTCAGA
       :::: .::     :.:::::::: :: ::::::::  ::::::::::: :::::::.::::::::::::::::
Mur.   ---CCTTGTCCAGTGTGGCTGACCC-TTGACCTCTTCCTTCCTCC---TCCCTTTGTTTTGGGATTCAGA
         2930      2940      2950      2960      2970      2980      2990

       3020      3030      3040.     3050      3060      3070      3080
Hvm.   AAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAAAAAAAAAAAAAAAAAAAA
       :::::::::::::: :::  :.:::::::::::::::::::                 :.:.:.::
Mur.   AAACTGCTTGTCACAGACAATTTATTTTTTATTAAAAA-------------------AGATATAA
        3000      3010      3020                              3030

       3090      3100
Hvm.  .AAAAAAAAGGGCGGCCGC
       . ...::::
Mur..  GCTTTAAAG---------
       3040
```

Fig. 3I
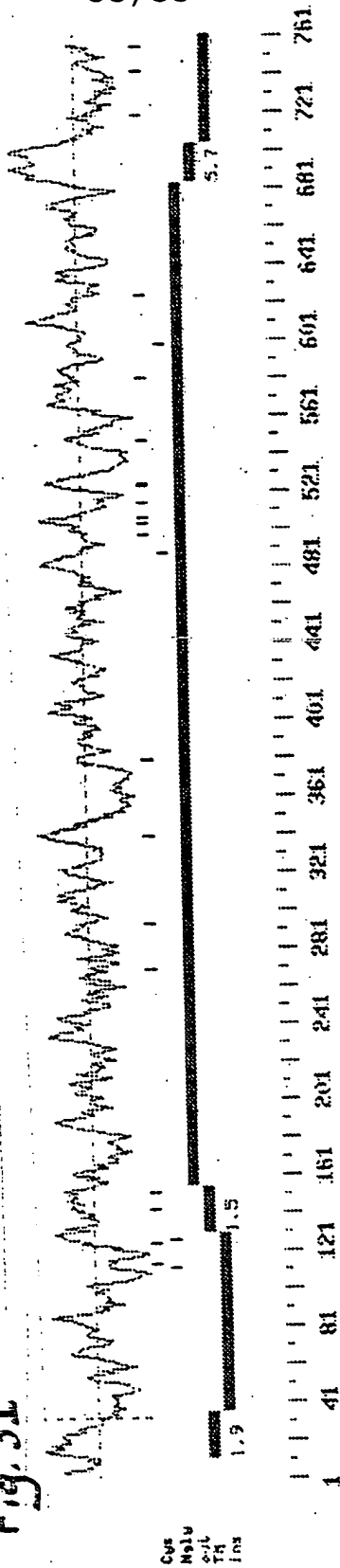
Fig. 4A

```
GTCGACCCACGCGTCCGCGGACGCGTGGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCGCCCCGCGCGGGGGCCGAGTC 79


                                                          M   R   R   Q   P   A    6
          GCGAAGCGCGCCTGCGACCCGGCGTCCGGGCGCGCTGGAGAGGACGCGAGGAGCC ATG AGG CGC CAG CCT GCG 152

  K   V   A   A   L   L   L   G   L   L   L   E   C   T   E   A   K   K   H   C   26
 AAG GTG GCG GCG CTG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC 212

  W   Y   F   E   G   L   Y   P   T   Y   Y   I   C   R   S   Y   E   D   C   C   46
 TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT 272

  G   S   R   C   C   V   R   A   L   S   I   Q   R   L   W   Y   F   W   F   L   66
 GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGG TTC CTT 332

  L   M   M   G   V   L   F   C   C   G   A   G   F   F   I   R   R   R   M   Y   86
 CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC 392

  P   P   P   L   I   E   E   P   A   F   N   V   S   Y   T   R   Q   P   P   N   106
 CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT 452

  P   G   P   G   A   Q   Q   P   G   P   P   Y   Y   T   D   P   G   G   P   G   126
 CCC GGC CCA GGA GCC CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG 512

  M   N   P   V   G   N   S   M   A   M   A   F   Q   V   P   P   N   S   P   Q   146
 ATG AAC CCT GTC GGG AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG 572

  G   S   V   A   C   P   P   P   P   A   Y   C   N   T   P   P   P   P   Y   E   166
 GGG AGT GTG GCC TGC CCG CCC CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA 632

  Q   V   V   K   A   K   *   173
 CAG GTA GTG AAG GCC AAG TAG   653


TGGGGTGCCCACGTGCAAGAGGAGAGACAGGAGAGGGCCTTTCCCTGGCCTTTCTGTCTTCGTTGATGTTCACTTCCAG   732

GAACGGTCTCGTGGGCTGCTAAGGGCAGTTCCTCTGATATCCTCACAGCAAGCACAGCTCTCTTTCAGGCTTTCCATGG   811

AGTACAATATATGAACTCACACTTTGTCTCCTCTGTTGCTTCTGTTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGT   890

GGTGACAGTCCCCGAGGGCTGACGTCCTTACGGTGGCGTGACCAGATCTACAGGAGAGAGACTGAGAGGAAGAAGGCAG   969

TGCTGGAGGTGCAGGTGGCATGTAGAGGGGCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCCGGGTATTAATAGG   1048

AAGCCCCATGCCGGGCGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCCAGCAGGTCATCTGCTCCAGCCTGT   1127

CCTCTCGTCAGCCTTCCTCTTCCAGAAGCTGTTGGAGAGACATTCAGGAGAGAGCAAGCCCCTTGTCATGTTTCTGTCT   1206

CTGTTCATATCCTAAAGATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC   1285

CTAGAATCAGGCTTGCCTTGGAGGCCTGACAGTGATCTGACATCCACTAAGCAAATTTATTTAAATTCATGGGAAATCA   1364

CTTCCTGCCCCAAACTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTTG   1443

GTGTGTTTATGGAAGTGCATGTAGAGCGTCCTGCCCTTTGAAATCAGACTGGGTGTGTGTCTTCCCTGGACATCACTGC   1522

CTCTCCAGGGCATTCTCAGGCCCGGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGGTTCTGAAGGGTGCTTTCAAA   1601

ACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGAGAGACCAGCTGAGGCGTCTCTCTCTGAGGTTGT   1680
```

GTTGGGTCTAAGCGGGTGTGTGCTGGGCTCCAAGGAGGAGGAGCTTGCTGGGAAAAGACAGGAGAAGTACTGACTCAAC 1759

TGCACTGACCATGTTGTCATAATTAGAATAAAGAAGAAGTGGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA 1838

CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGAGCTAGTTCCGCCGCATAGTTATAGTGTTGA 1917

TGTGTGAACGCTGACCTGTCCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCGCCTAGATTACTAGATGTGCTGTAT 1996

CACGGGGAATGAGGTGGGGGTGCTTATTTTTTAATGAACTAATCAGAGCCTCTTGAGAAATTGTTACTCATTGAACTGG 2075

AGCATCAAGACATCTCATGGAAGTGGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG 2154

AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAACAGACACCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233

CCACCAGTGTCTCTGACCACCCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCTCCATCTAAA 2312

TGAGACAACAAAGCACAATGTTCACTGTTTACAACCAAGACAACTGCGTGGGTCCAAACACTCCTCTTCCTCCAGGTCA 2391

TTTGTTTTGCATTTTTAATGTCTTTATTTTTTGTAATGAAAAAGCACACTAAGCTGCCCCTGGAATCGGGTGCAGCTGA 2470

ATAGGCACCCAAAAGTCCGTGACTAAATTTCGTTTGTCTTTTTGATAGCAAATTATGTTAAGAGACAGTGATGGCTAGG 2549

GCTCAACAATTTTGTATTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACTTGGTTAGAATTGTGCTACTGT 2628

GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCCTGGCCATTCTTGTTTCCATTGTGTGGATGGTGGG 2707

TTGTGCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG 2786

CAGATCTGTGCATGCTTTTCCTCTGCAACAATTGGCTCGTTTCTCTTTTTGTTCTCTTTTGATAGGATCCTGTTTCCT 2865

ATGTGTGCAAAATAAAAATAAATTTGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2944

AAAAAAAAAAGGGCGGCCGC   2964

Fig. 4B

Fig. 4C

```
GTCGACCCACGCGTCCGGCCGCGCGTCCTTCTGCCGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCCGTCCCGGGGT   79


                                                              M   G   R   R   L     5
GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCTCGCTGGAGCC ATG GGC CGC CGG CTC    151

  G   R   V   A   A   L   L   L   G   L   L   V   E   C   T   E   A   K   K   H    25
 GGC AGG GTG GCG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT  211

  C   W   Y   F   E   G   L   Y   P   T   Y   Y   I   C   R   S   Y   E   D   C    45
 TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC  271

  C   G   S   R   C   C   V   R   A   L   S   I   Q   R   L   W   Y   F   W   F    65
 TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC  331

  L   L   M   M   G   V   L   F   C   C   G   A   G   F   F   I   R   R   R   M    85
 CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC TTC ATT CGC CGG CGC ATG  391

  Y   P   P   P   L   I   E   E   P   T   F   N   V   S   Y   T   R   Q   P   P   105
 TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA  451

  N   P   A   P   G   A   Q   Q   M   G   P   P   Y   Y   T   D   P   G   G   P   125
 AAT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC  511

  G   M   N   P   V   G   N   T   M   A   M   A   F   Q   V   Q   P   N   S   P   145
 GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT  571

  H   G   G   T   T   Y   P   P   P   P   S   Y   C   N   T   P   P   P   P   Y   165
 CAC GGA GGC ACA ACT TAC CCA CCC CCT CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT  631

  E   Q   V   V   K   D   K   *                                                   173
 GAA CAG GTG GTG AAG GAC AAG TAG                                                  655

CAAGATGCTACATCAAAGGCAAAGAGGATGGACAGGCCCTTTTGTTTACCTTCCCATCCTCACCGATACTTGCTGATAG   734

GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCCAGCTCTCTTTCAAGTCTTTTGTGGAGGACATTTGAATC   813

CACACTGTCTCCTCTGTTGCTTCTGTTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCTGAGGGTT   892

GATATTCCTAGGGTGTCCAGGGTAGATCCTCGGGAGAGAGGCTAAGGGGAAAGGAAGGCATAGCCTGTGTGTTAGGGGG   971

CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGACACTATCCACCA  1050

TCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG  1129

GCTTTCCTCTGCAGGAATAGGAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG  1208

TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGACATT  1287

GCGTTTTATGAATCATCGTCTGGCTTTTCTTTTAGTGCATGTATTGAAGTGAGGGTGTCCTTTGAGATCAGATGGGGAG  1366

AGTGAACTCTGCGGGGGGTGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTCTTAGGTAGTTCTGGTGATGGGTT  1445

TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAAGAGGACAGCCAAAG  1524
```

AAACTCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA   1603

GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAGTAGAGAAAGAAG   1682

TGTAGTTAGAGATGCCATTTCCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA   1761

TGGAGTTCTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA   1840

GGAAGTATAGCTAAGATGTCTAGATTATTTATATGTAGTATGGTGGGGAGTGGGGCTGCAAGGAAGGGGGCTGACATTG   1919

TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT   1998

GAGTATTCTTTACCACCTACAAGACCAGGAGGCATGGTGTCATTCTCCATTGGGGTATTTATATGAGGTAGAGGTTCAG   2077

GAATCGACAGTAGCTGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG   2156

GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCTTGTGTCTCTGGC   2235

TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGTTTTACATAAGACAACAAAGCACAATGTCTGCTGTT   2314

TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTCTTCTATCACTTGTGGCTTTAACTTCCATTTCCTCCGTT   2393

CCTTTTTAAAATCAAGAAGCACAGTCAGAGCTGCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC   2472

CATGACTAAATCTTATCTTTTTGATAGCAAATCCTTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTTATACTC   2551

CAATGTCTGTGTAAGGTAAATTTTGTTTGCCATTGAGCCCACATTGGAATTCCTTCTGACGTCAACACTGACAATGCCT   2630

ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC   2709

AGCTCTACTTCTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTTC   2788

TTGGCAACACTTGGCTCATATTTCTTGTTCTCTTTTGATAGAGTCCTGTTTCCTATGTATTTAAAAAATAATAAAAGTG   2867

AATTTAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC   2915

Fig. 4D

Fig. 4E

```
              10        20        30        40        50        60        70
Hum.  MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG
      : :. ..:::::::::.::::::::::::::::::::::::::::::::::::::::::::::::::::
Mur.  MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG
              10        20        30        40        50        60        70


              80        90       100       110       120       130       140
Hum.  VLFCCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV
      :::::::::::::::::::::::::.:::::::::::::.::::: :::::::::::::::::.::::::::
Mur.  VLFCCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPPNPAPGAQQMGPPYYTDPGGPGMNPVGNTMAMAFQV
              80        90       100       110       120       130       140


              150       160       170
Hum.  PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK
      .:::::...... :::::.:::::::::::::.:
Mur.  QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK
              150       160       170
```

Fig. 4F
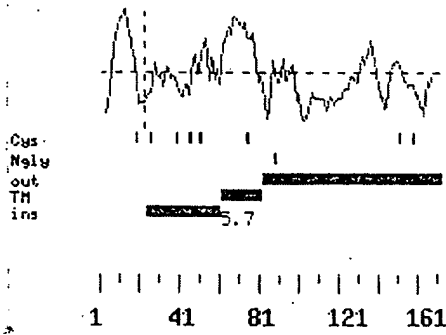
Fig. 4G
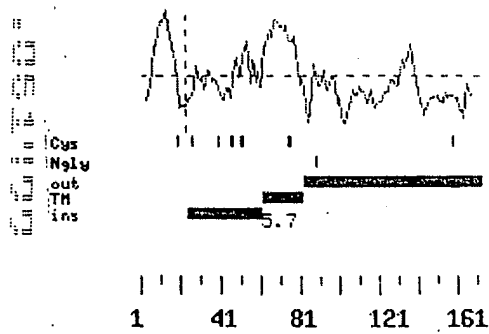
Fig.5A

```
GTCGACCCACGCGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA   79
```

```
                                                        M   C   T   K   T   I     6
TCAAGAAAGGCCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC   150
```

```
 P   V   L   W   G   C   F   L   L   W   N   L   Y   V   S   S   S   Q   T   I    26
CCA GTC CTC TGG GGA TGT TTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT   210
```

```
 Y   P   G   I   K   A   R   I   T   Q   R   A   L   D   Y   G   V   Q   A   G    46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GTT CAA GCT GGA   270
```

```
 M   K   M   I   E   Q   M   L   K   E   K   K   L   P   D   L   S   G   S   E    66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG   330
```

```
 S   L   E   F   L   K   V   D   Y   V   N   Y   N   F   S   N   I   K   I   S    86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT   390
```

```
 A   F   S   F   P   N   T   S   L   A   F   V   P   G   V   G   I   K   A   L   106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA   450
```

```
 T   N   H   G   T   A   N   I   S   T   D   W   G   F   E   S   P   L   F   V   126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT   510
```

```
 L   Y   N   S   F   A   E   P   M   E   K   P   I   L   K   N   L   N   E   M   146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG   570
```

```
 L   C   P   I   I   A   S   E   V   K   A   L   N   A   N   L   S   T   L   E   166
CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG   630
```

```
 V   L   T   K   I   D   N   Y   T   L   L   D   Y   S   L   I   S   S   P   E   186
GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA   690
```

```
 I   T   E   N   Y   L   D   L   N   L   K   G   V   F   Y   P   L   E   N   L   206
ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC   750
```

```
 T   D   P   P   F   S   P   V   P   F   V   L   P   E   R   S   N   S   M   L   226
ACC GAC CCC CCC TTC TCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC   810
```

```
 Y   I   G   I   A   E   Y   F   F   K   S   A   S   F   A   H   F   T   A   G   246
TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG   870
```

```
 V   F   N   L   T   L   S   T - E   E   I   S   N   H   F   V   Q   N   S   Q   266
GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA   930
```

```
 G   L   G   N   V   L   S   R   I   A   E   I   Y   I   L   S   Q   P   F   M   286
GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG   990
```

```
 V   R   I   M   A   T   E   P   P   I   I   N   L   Q   P   G   N   F   T   L   306
GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG  1050
```

```
 D   I   P   A   S   I   M   M   L   T   Q   P   K   N   S   T   V   E   T   I   326
GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC  1110
```

```
 V   S   M   D   F   V   A   S   T   S   V   G   L   V   I   L   G   Q   R   L   346
```

```
GTT TCC ATG GAC TTC GTT GCT AGT ACC AGT GTT GGC CTG GTT ATT TTG GGA CAA AGA CTG   1170

 V   C   S   L   S   L   N   R   F   R   L   A   L   P   E   S   N   R   S   N    366
GTC TGC TCC TTG TCT CTG AAC AGA TTC CGC CTT GCT TTG CCA GAG TCC AAT CGC AGC AAC   1230

 I   E   V   L   R   F   E   N   I   L   S   S   I   L   H   F   G   V   L   P    386
ATT GAG GTC TTG AGG TTT GAA AAT ATT CTA TCG TCC ATT CTT CAC TTT GGA GTC CTC CCA   1290

 L   A   N   A   K   L   Q   Q   G   F   P   L   P   N   P   H   K   F   L   F    406
CTG GCC AAT GCA AAA TTG CAG CAA GGA TTT CCT CTG CCC AAT CCA CAC AAA TTC TTA TTC   1350

 V   N   S   D   I   E   V   L   E   G   F   L   L   I   S   T   D   L   K   Y    426
GTC AAT TCA GAT ATT GAA GTT CTT GAG GGT TTC CTT TTG ATT TCC ACC GAC CTG AAG TAT   1410

 E   T   S   S   K   Q   Q   P   S   F   H   V   W   E   G   L   N   L   I   S    446
GAA ACA TCC TCA AAG CAG CAG CCA AGT TTC CAC GTA TGG GAA GGT CTG AAC CTG ATA AGC   1470

 R   Q   W   R   G   K   S   A   P   *                                           456
AGA CAG TGG AGG GGG AAG TCA GCC CCT TGA                                          1500

TTGCCGGTTTGCAATTCACCCCAGGAAGTAAATGGTCCTTAATCCTACAACTACTGTAAACCCAGAAGGGAAAGACAGT   1579

AGACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTTCTTTCTTAAGCCTTCAGGAACCCAGAATAA   1658

GGCAGACTCTGTTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTGTCTGTGTTTATGTTTG   1737

TTTGTTTGTTTGGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG   1816

TCTGTATTTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCCCTACCTGCATATTGGTTTTC   1895

ATGTTTTATATTCACTGTTACTATCTTCTGTGTTTAATTAAAATTGTTTTCTATCAAAAAAAAAAAAAAAAAAAAAGGGC   1974

GGCCGC                                                                          1980
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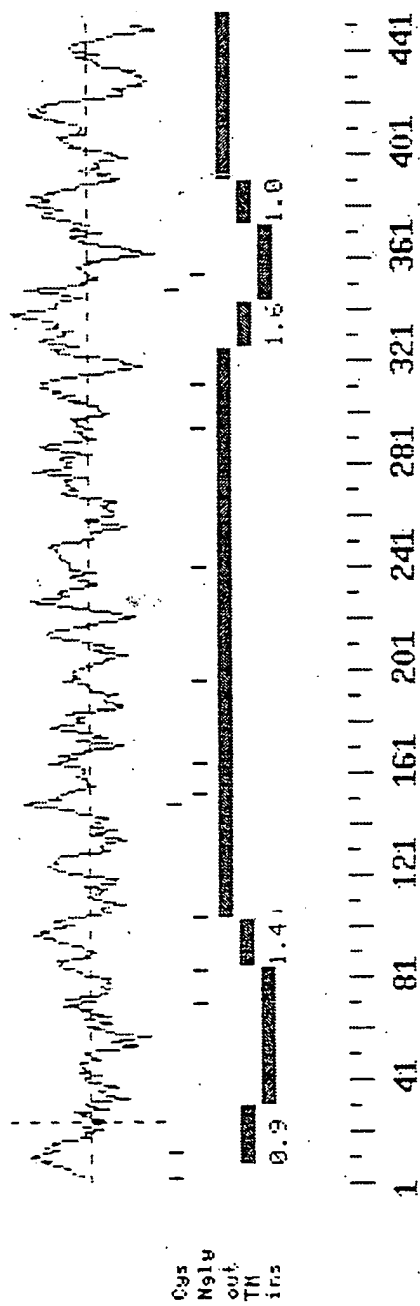
Fig. 5B

Fig. 5C

Fig. 5D

```
              10        20        30        40        50         60
286  MCTKT-IPVLWGCFL-LWNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL
     :      .  :  .. : .. .. .. .. ::. .::.:..::. : :    ... :: :..:: : ..:.
BPI  MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
              10        20        30        40        50        60

     70        80        90        100       110       120       130
286  EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
     :  .. .. .:.: .. : .: .:.. .. ::.:.:.: ..... .:: :  .  .. .. ..:. ..:
BPI  KIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM
     70        80        90          100       110       120       130

                                                         140       150
286  ----------------KPI---------------------------------LKN-LNEMLCPIIASE
                     ::.                                  :.: .:  .: ...
BPI  SISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
     140       150       160       170       180       190       200

        160       170       180       190       200       210       220
286  VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN
     :  : ..  :: :.:.:::.  .:.:..:: ...... ::..:: .. : .. :::.:   ..: .
BPI  VSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHD
     210       220       230       240       250       260       270

        230       240       250       260       270       280       290
286  SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNH--FVQNSQGLGNVLSRIAEIYILSQPFMVRIMA
     :.:.:..::..::..:...   :::.:..::  . :..    :   ... .:. :. .:    . .... :
BPI  RMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFP-NMKIQIHVSA
     280       290       300       310       320       330       340

        300       310       320       330       340       350       360
286  TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRLALPE
     . : ...::  .:     :::.. ..  .. : .  .:::: : :.: .:. :.:
BPI  STPPHLSVQPTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKH
     350       360       370       380       390       400       410

        370       380       390       400       410       420       430
286  SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK
     ::    : :  ..:..  :.  ::: .:.:::.:..:: ..   ..  .. .. ..:.::.:: .
BPI  SNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVYK----
     420       430       440       450       460       470       480

        440       450
286  QQPSFHVWEGLNLISRQWRGKSAP -

     -----------------------
```

Fig.5E

```
                10        20        30        40        50        60
  286  MCTKTIPVLWGCFLLWNLYVSSSQTI--YPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL
       :  :  ..      ..::  :  .:...   ::. :::::..:.:..::.  ..  :   :::..: ..:
 RENP  MGALARAL--PSILLALLLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
                10        20        30        40        50        60


                70        80        90       100       110       120       130
  286  EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
       .  :.     :.:  ...: .:  .:..  .. ::.::.:    .....  .::  :   .  .. ..: ...:
 RENP  RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM
                70        80        90       100       110       120       130


                                                               140       150
  286  ------------------KPI------------------------------------LKN-LNEMLCPIIASE
                        ::.                                     :.:  .:   ...
 RENP  SISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
          140       150       160       170       180       190       200


                160       170       180       190       200       210       220
  286  VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN
       : .:.   .  :: ..:     .. :.. :. :..::.: :::..::  ::  ::.  :  :::.:  .::  . 
 RENP  VSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHD
          210       220       230       240       250       260       270


                230       240       250       260       270       280       290
  286  SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNH--FVQNSQGLGNVLSRIAEIYILSQPFMVRIMA
       :.:.:...:::..:...  .  :::...::   . :..   :  ... .:. :.  .:     . ...  :
 RENP  RMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFP-NMKIQIHVSA
          280       290       300       310       320       330       340


                300       310       320       330       340       350       360
  286  TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRLALPE
       . ::  ...::  ..:.    ....    .:  :: :.....   ..   :.. :   ..::: :.:..: :.:
 RENP  STPPHLSVQPTGLTFYPAVDVQALAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKH
          350       360       370       380       390       400       410


                370       380       390       400       410       420       430
  286  SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK
       ::   ..     .   ..  . :::  .:.::::.:   :   .:.:....:::.:   .::::.::. .  :
 RENP  SNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVYK----
          420       430       440       450       460       470       480


                440       450
  286  QQPSFHVWEGLNLISRQWRGKSAP

       ------------------------
```

Fig. 6A

```
GTCGACCCACGCGTCCGGGGAATTGCAGCAGGAAAATATGTGAAGAGTTTTTAAACCCACAAATTCTTCTTACTTTAGA   79

                                              M   L   E   T   L   S   R   Q    8
ATTAGTTGTTACATTGGCAGGAAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG  149

 W   I   V   S   H   R   M   E   M   W   L   L   I   L   V   A   Y   M   F   Q   28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG  209

 R   N   V   N   S   V   H   M   P   T   K   A   V   D   P   E   A   F   M   N   48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT  269

 I   S   E   I   I   Q   H   Q   G   Y   P   C   E   E   Y   E   V   A   T   E   68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA  329

 D   G   Y   I   L   S   V   N   R   I   P   R   G   L   V   Q   P   K   K   T   88
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA  389

 G   S   R   P   V   V   L   L   Q   H   G   L   V   G   G   A   S   N   W   I  108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT  449

 S   N   L   P   N   N   S   L   G   F   I   L   A   D   A   G   F   D   V   W  128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG  509

 M   G   N   S   R   G   N   A   W   S   R   K   H   K   T   L   S   I   D   Q  148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA  569

 D   E   F   W   A   F   S   Y   D   E   M   A   R   F   D   L   P   A   V   I  168
GAT GAG TTC TGG GCT TTC AGT TAT GAT GAG ATG GCT AGG TTT GAC CTT CCT GCA GTG ATA  629

 N   F   I   L   Q   K   T   G   Q   E   K   I   Y   Y   V   G   Y   S   Q   G  188
AAC TTT ATT TTG CAG AAA ACG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC  689

 T   T   M   G   F   I   A   F   S   T   M   P   E   L   A   Q   K   I   K   M  208
ACC ACC ATG GGC TTT ATT GCA TTT TCC ACC ATG CCA GAG CTG GCT CAG AAA ATC AAA ATG  749

 Y   F   A   L   A   P   I   A   T   V   K   H   A   K   S   P   G   T   K   F  228
TAT TTT GCT TTA GCA CCC ATA GCC ACT GTT AAG CAT GCA AAA AGC CCC GGG ACC AAA TTT  809

 L   L   L   P   D   M   M   I   K   G   L   F   G   K   K   E   F   L   Y   Q  248
TTG TTG CTG CCA GAT ATG ATG ATC AAG GGA TTG TTT GGC AAA AAA GAA TTT CTG TAT CAG  869

 T   R   F   L   R   Q   L   V   I   Y   L   C   G   Q   V   I   L   D   Q   I  268
ACC AGA TTT CTC AGA CAA CTT GTT ATT TAC CTT TGT GGC CAG GTG ATT CTT GAT CAG ATT  929

 C   S   N   I   M   L   L   L   G   G   F   N   T   N   N   M   N   M   S   R  288
TGT AGT AAT ATC ATG TTA CTT CTG GGT GGA TTC AAC ACC AAC AAT ATG AAC ATG AGC CGA  989

 A   S   V   Y   A   A   H   T   L   A   G   T   S   V   Q   N   I   L   H   W  308
GCA AGT GTA TAT GCT GCC CAC ACT CTT GCT GGA ACA TCT GTG CAA AAT ATT CTA CAC TGG 1049

 S   Q   A   V   N   S   G   E   L   R   A   F   D   W   G   S   E   T   K   N  328
AGC CAG GCA GTG AAT TCT GGT GAA CTC CGG GCA TTT GAC TGG GGG AGT GAG ACC AAA AAT 1109

 L   E   K   C   N   Q   P   T   P   V   R   Y   R   V   R   D   M   T   V   P  348
```

CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

```
   T   A   M   W   T   G   G   Q   D   W   L   S   N   P   E   D   V   K   M   L   368
ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229
```

```
   L   S   E   V   T   N   L   I   Y   H   K   N   I   P   E   W   A   H   V   D   388
CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289
```

```
   F   I   W   G   L   D   A   P   H   R   M   Y   N   E   I   I   H   L   M   Q   408
TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349
```

```
   Q   E   E   T   N   L   S   Q   G   R   C   E   A   V   L   *               424
CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA                 1397
```

AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAATTACGGAGAGCA 1476

GAGACCTAGTATACATTTTTCAGATTCCCTGCACTTGGCACTAAATCCGACACTTACATTTACATTTTTTTTCTGTAAA 1555

TTAAAGTACTTATTAGGTAAATAGAGGTTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTTACCTGAT 1634

AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTTAAAACACCTATTGTTTTTTCTATAAGCCAT 1713

ATTTTTGGAGCACTAAAGTAAAATGGCAAATTGGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA 1792

CAAAATAAGCTAGACATTTTCACCTTGTTGCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA 1871

CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTCTCAGAATAAGGCCAAGTTTTATAGTTGCA 1950

TGTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAAAAAAAAAAA 2029

AAAAAGGGCGGCCGC 2044

Fig. 6B

Fig.6C

```
            10        20        30        40        50        60        70
294  MLETLSRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIQHQGYPCEEYEVATEDG
     :         :..    .  :  ::  :  .     . .:    . .::. :::::..:   ::: :::::::.:::
HLP  M-------WLL---LTMASLISVLGTTHGLFGKLH----PGSPEVTMNISQMITYWGYPNEEYEVVTEDG
             10        20            30        40        50

            80        90       100       110       120       130       140
294  YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWSRK
     :::  ::::::  ::.   :: :::::::::::::::::::::::::::::::::::::.::.::::::::.:.
HLP  YILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWISNLPNNSLAFILADAGYDVWLGNSRGNTWARR
            60        70        80        90       100       110       120

           150       160       170       180       190       200       210
294  HKTLSIDQDEFWAFSYDEMARFDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKMYF
     .":  :::::::::::::::::.::::.::    .. ::: ::::::::::::: : ::..:: ..
HLP  NLYYSPDSVEFWAFSFDEMAKYDLPATIDFIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFY
           130       140       150       160       170       180       190

           220       230       240       250       260       270
294  ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF
     :::::.:::: ..::   .: ...:.  .:: .:  : :  .. :.  :: .::: ..::   .... ::
HLP  ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
           200       210       220       230       240       250       260

    280       290       300       310       320       330       340
294  NTNNMNMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
    ...: : :: .:: .:. :::::::.::.:::..:: ..:.::: ..:   :: : :  : .:.:.
HLP  DSKNFNTSRLDVYLSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPI
    270       280       290       300       310       320       330

    350       360       370       380       390       400       410
294  AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGRC
    :.:.::.:.:: ..::: .::.   . :::::::: .:.:::::.::. .:::... ..
HLP  AVWNGGKDLLADPQDVGLLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-------
    340       350       360       370       380       390

    420
294  EAVL

HLP  ----
```

Fig.6D

Fig. 6E

```
                  10        20        30        40        50        60
294   MLETLSRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTK--AVDPEAFMNISEIIQHQGYPCEEYEVATE
      :            :..: ::..   . ...:      :   :::::. ::..:::     :.: ::: :..:
LAL   M-------------KMRFLGLVVCLVLWPLHSEGSGGKLTAVDPETNMNVSEIISYWGFPSEEYLVETE
                            10        20        30        40        50


      70        80        90       100       110       120       130
294   DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS
      ::::: .::::.:  .      :..:::.:.:::....::.::.::.:.:::::::::::::::::.::
LAL   DGYILCLNRIPHGRKNHSDKGPKPVVFLQHGLLADSSNWVTNLANSSLGFILADAGFDVWMGNSRGNTWS
        60        70        80        90       100       110       120


      140       150       160       170       180       190       200
294   RKHKTLSIDQDEFWAFSYDEMARFDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKM
      :::::::.: ::::::::::::::. ::::::: :::::::. :::::.:::::.:::::.: ::::..::
LAL   RKHKTLSVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQVYYVGHSQGTTIGFIAFSQIPELAKRIKM
        130       140       150       160       170       180       190


     210       220       230       240       250       260       270
294  YFALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGG
     .::::.:.:.:     ::  :::   ::: .:::.:: :::: :: .:.:::::.:::::.: .: :
LAL  FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKEFLPQSAFLKWLGTHVCTHVILKELCGNLCFLLCG
       200       210       220       230       240       250       260


     280       290       300       310       320       330       340
294  FNTNNMNMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
     ::  :.:::::..:::.. :. :::::::::::::::.   ..::::: .::    ::. . : :.:: ::
LAL  FNERNLNMSRVDVYTTHSPAGTSVQNMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDMLVP
       270       280       290       300       310       320       330


     350       360       370       380       390       400       410
294  TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
     :::.::.:::..   ::..:.:::.:: .:::::.:::.:.:::::::::::.: .:: ::..:.. .
LAL  TAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKIINLMRKYQ-------
       340       350       360       370       380       390


     420
294  CEAVL

LAL  -----
```

Fig. 7A

```
                                                                          M   A      2
GTCGACCCACGCGTCCACGGCGAGGGCTCCCGGGGGCGCAGCATTGCCCCCCCTGCACCACCTCACCAAG ATG GCT     75

   T   L   G   H   T   F   P   F   Y   A   G   P   K   P   T   F   P   M   D   T      22
  ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC    135

   T   L   A   S   I   I   M   I   F   L   T   A   L   A   T   F   I   V   I   L      42
  ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG    195

   P   G   I   R   G   K   T   R   L   F   W   L   L   R   V   V   T   S   L   F      62
  CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC    255

   I   G   A   A   I   L   A   V   N   F   S   S   E   W   S   V   G   Q   V   S      82
  ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC    315

   T   N   T   S   Y   K   A   F   S   S   E   W   I   S   A   D   I   G   L   Q     102
  ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG    375

   V   G   L   G   G   V   N   I   T   L   T   G   T   P   V   Q   Q   L   N   E     122
  GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG    435

   T   I   N   Y   N   E   E   F   T   W   R   L   G   E   N   Y   A   E   E   C     142
  ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT    495

   A   K   A   L   E   K   G   L   P   D   P   V   L   Y   L   A   E   K   F   T     162
  GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT    555

   P   R   S   P   C   G   L   Y   R   Q   Y   R   L   A   G   H   Y   T   S   A     182
  CCA AGA AGC CCA TGT GGC CTA TAC CGC CAG TAC CGC CTG GCG GGA CAC TAC ACC TCA GCC    615

   M   L   W   V   A   F   L   C   W   L   L   A   N   V   M   L   S   M   P   V     202
  ATG CTA TGG GTG GCA TTC CTC TGC TGG CTG CTG GCC AAT GTG ATG CTC TCC ATG CCT GTG    675

   L   V   Y   G   G   Y   M   L   L   A   T   G   I   F   Q   L   L   A   L   L     222
  CTG GTA TAT GGT GGC TAC ATG CTA TTG GCC ACG GGC ATC TTC CAG CTG TTG GCT CTG CTC    735

   F   F   S   M   A   T   S   L   T   S   P   C   P   L   H   L   G   A   S   V     242
  TTC TTC TCC ATG GCC ACA TCA CTC ACC TCA CCC TGT CCC CTG CAC CTG GGC GCT TCT GTG    795

   L   H   T   H   H   G   P   A   F   W   I   T   L   T   T   G   L   L   C   V     262
  CTG CAT ACT CAC CAT GGG CCT GCC TTC TGG ATC ACA TTG ACC ACA GGA CTG CTG TGT GTG    855

   L   L   G   L   A   M   A   V   A   H   R   M   Q   P   H   R   L   K   A   F     282
  CTG CTG GGC CTG GCT ATG GCG GTG GCC CAC AGG ATG CAG CCT CAC AGG CTG AAG GCT TTC    915

   F   N   Q   S   V   D   E   D   P   M   L   E   W   S   P   E   E   G   G   L     302
  TTC AAC CAG AGT GTG GAT GAA GAC CCC ATG CTG GAG TGG AGT CCT GAG GAA GGT GGA CTC    975

   L   S   P   R   Y   R   S   M   A   D   S   P   K   S   Q   D   I   P   L   S     322
  CTG AGC CCC CGC TAC CGG TCC ATG GCT GAC AGT CCC AAG TCC CAG GAC ATT CCC CTG TCA   1035

   E   A   S   S   T   K   A   Y   C   K   E   A   H   P   K   D   P   D   C   A     342
  GAG GCT TCC TCC ACC AAG GCA TAC TGT AAG GAG GCA CAC CCC AAA GAT CCT GAT TGT GCT   1095
```

```
  L     *                                                                    344
TTA  TAA                                                                    1101

CATTCCTCCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCATTGGCGCCCCATAAAACCAGCAGAACTG   1180

CCCTCAGGGTGGCTGTTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT   1259

AAAAAACAAAACAAAACAAAAAGCCCTAAGGGACTGAAGAGATGCTGGGCCTGTCCATAAAGCCTGTTGCCATGATAAG   1338

GCCAAGCAGGGGCTAGCTTATCTGCACAGCAACCCAGCCTTTCCGTGCTGCCTTGCCTCTTCAAGATGCTATTCACTGA   1417

AACCTAACTTCACCCCCATAACACCAGCAGGGTGGGGGTTACATATGATTCTCCTATGGTTTCCTCTCATCCCTCGGCA   1496

CCTCTTGTTTTCCTTTTTCCTGGGTTCCTTTTGTTCTTCCTTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA   1575

AGACAGCACTGGAAAGGAGGGGAAACCAAACTTCTCATCCTAGGTCTAACATTAACCAACTATGCCACATTCTCTTTGA   1654

GCTTCAGTTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAATCTTGGGATTTATCTTTCTATGCCTTGCTGA   1733

CACCTACCTTGGCCCTCAAACACCACCTCACAAGAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT   1812

TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGGAGTGGGTGACCTGCCTCATCACTGCCACCTAA   1891

CGTCCCCCTGGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCTCACTAGAGGGCGCCCCTATTACTC   1970

TGGAGTCGACGCAGAGAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCAGCGAAGCTCATGA   2049

GGACGTGCGACCCCGGCGCGGAGAAGCCATGAAAATTAATGGGAAAAACAGTTTTTAAAAAAAAAAAAAAAAAAAGGGCG   2128

GCCGC                                                                       2133
```

Fig. 7B

Fig. 7C

Fig. 7D

```
              10        20        30        40        50        60        70
296  MATLGHTFPFYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILAV
     :   ..:   :..  ..    ::.  .:!..  ..:.::!.:  . .   :   :  .:.:.:
CRP  M-RIAH-----ASSRGNI-------SIFSVFLIPLIAYILILPGVR-RKRVVTTVTYVLMLAVGGALIAS
                  10                 20        30        40        50


              80        90        100       110             120       130
296  NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL------TGTPVQQLNETIN--YNEEFTW
     .  .: :   .: ..  ::!.: :  ::...:: ::.::    ...:  ..   ::: :
CRP  LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNEGFDI
        60        70        80        90        100       110       120


              140       150       160       170       180       190       200
296  RLGENYAEECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM
     .  ::.    .::.:.::  ..:  .:  .  ... . :.::.:.:::! : .: :: :: :.  .
CRP  SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLSVVLMLFL
        130       140       150       160       170       180       190


              210       220       230       240       250       260
296  PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLHTHHGPAF----WITLTTGLLCVL
     :  .: .  .::::: :.:  :  :  : :::  :..  :..   ...  ..:   ....:.:::
CRP  PHNAYKS--ILATGISCLIACLVYL----LLSPCELRIAFTGENFERVDLTATFSFCFYLIFAIGILCVL
        200       210            220       230       240       250       260


              270       280       290       300       310       320
296  LGLAMAVAHRMQPHRLKAFFNQSVDEDPMLEW------SPEEGGLLSPRY--RSMADSPKSQDIPLSEAS
     ::....  . .   : .::. :.::.   :        .:.  :.    :    . ...:   .::. . ..
CRP  CGLGLGICEHWRIYTLSTFLDASLDEHVGPKWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA
                 270       280       290       300       310       320       330


         330                      340
296  STKAY------CK------------EAHPKDPD-----------CA---L
     .. ..      :.            :.   ...            :.
CRP  GSSGFQSRTSTCQSSASSASLRSQSSIETVHDEAELERTHVHFLQEPCSSSST
         340       350       360       370       380
```